

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:46:10 ; Search time 5.42903 Seconds
(without alignments)
904.569 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

Sequence: 1 gcaatgatggggcattctt.....ccatcaagaagatttggtt 297

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ASSWEB_spool/US10079954/runat_23032006_102933_1875/app_query.fasta_1
-DB=Issued Patents AA -QFMT=faatan -SUFFIX=rai -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	80.3	233	2	US-09-148-545-137
2	453	80.3	233	2	US-09-621-011-137
3	453	80.3	241	2	US-08-808-148-1
4	453	80.3	241	2	US-09-020-956-114
5	453	80.3	241	2	US-09-030-607-114
6	453	80.3	241	2	US-09-439-313-114
7	453	80.3	241	2	US-09-352-616A-114
8	453	80.3	241	2	US-09-232-149A-114
9	453	80.3	241	2	US-09-159-812-114
10	453	80.3	241	2	US-09-636-215-114
11	453	80.3	241	2	US-09-685-166A-114
12	453	80.3	241	2	US-09-115-453-114

ALIGNMENTS

RESULT 1

US-09-148-545-137
; Sequence 137, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23

Sequence 114, App
Sequence 114, App
Sequence 114, App
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Sequence 22, Appl
Sequence 443, App
Sequence 81, Appl
Sequence 79, Appl
Sequence 6334, Ap
Sequence 9861, Ap
Sequence 1, Appl
Sequence 4, Appl
Sequence 19, Appl
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Sequence 11243, A
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Sequence 216, App
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Sequence 3, Appl
Sequence 2, Appl
Sequence 10626, A
Sequence 1, Appl
Sequence 6, Appl

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/	EARLIER FILING DATE:	1997-08-22
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/	EARLIER FILING DATE:	1997-08-22
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/	EARLIER APPLICATION NUMBER:	60/056,637
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,903
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,888
/	EARLIER FILING DATE:	1997-08-22
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/	EARLIER FILING DATE:	1997-08-22
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/	EARLIER APPLICATION NUMBER:	60/056,894
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/	EARLIER APPLICATION NUMBER:	60/056,910
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/	EARLIER APPLICATION NUMBER:	60/056,864
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,631
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,845
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,892
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/047,595
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/057,761
/	EARLIER FILING DATE:	05-Sep-1997
/	EARLIER APPLICATION NUMBER:	60/047,599
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,588
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,585
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,586
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,590
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,594
/	EARLIER FILING DATE:	1997-04-11
/	EARLIER APPLICATION NUMBER:	60/047,589
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,593
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/047,614
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/043,578
/	EARLIER FILING DATE:	1997-04-11
/	EARLIER APPLICATION NUMBER:	60/043,576
/	EARLIER FILING DATE:	1997-04-11
/	EARLIER APPLICATION NUMBER:	60/047,501
/	EARLIER FILING DATE:	1997-05-23
/	EARLIER APPLICATION NUMBER:	60/043,670
/	EARLIER FILING DATE:	1997-04-11
/	EARLIER APPLICATION NUMBER:	60/056,632
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,664
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,876
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,881
/	EARLIER FILING DATE:	1997-08-22

US-10-079-954-1 (1-297) x US-09-621-011-137 (1-233)

121	CTGGCTGCTATGGTGTCTAAAGCTAGAGACGAGTGTCCCTCGTGACGTTCTTTTCATC	180
QY		
64	LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheIle	83
Db		
181	CTCCTCTCTCATCTTCATTGCTGAGGTTGCGAGCTGCTGTGGTGGCTTGGTGACACCATTA	240
QY		
84	LeuLeuLeuIlePheIleAlaGluValAlaAlaAlaValValAlaLeuValTyrThrThr	103
Db		
241	ATGGCTGAGACGATTCGCGAGCTTGCTGGTATGTGCTGCCATCAAGAAG	288
QY		
104	MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys	119
Db		

RESULT 3
US-08-808-148-1
; Sequence 1, Application US/08808148

;
 ; ADDRESS: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ;

[illegible]

```

? SEQ ID NO: 137
? LENGTH: 233
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (233)
? OTHER INFORMATION: Xaa equals stop translation
US-09-621-011-137
?
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
? TELEX:
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 241 amino acids
? TYPE: amino acid
? STRANDEDNESS: single

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US-09-621-011-137


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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-114

Alignment Scores:
Pred. No.: 9.61e-46 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 2 Gaps: 0

US-10-079-954-1 (1-297) x US-09-030-607-114 (1-241)
QY 1 GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAG 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
33 SerileaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52
QY 61 TTTGTCAACGTGGGCTACTTCTCATCGACGCCGGTGTGGTCTTTTGTCTTGGTTTC 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
53 PheValaenValGlyTyPheLeuIleAlaAaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCTGCTGCTTCTTCTTCATC 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
73 LeuGlyCysTyGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheile 92
QY 181 CTCCTCTCATCTTTCATTGCTGAGGTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValValAlaLeuValThrThrThr 112
QY 241 ATGGCTGAGCACTTCCCGACGTTTGGTGTAGTGCCTGCCATCAAGAAG 288
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
113 MetAlaGluHisPheLeuThrLeuValValProAlaIleLysLys 128

RESULT 7
US-09-352-616A-114
; Sequence 114, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillion, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-352-616A-114

Alignment Scores:
Pred. No.: 9.61e-46 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 2 Gaps: 0

US-10-079-954-1 (1-297) x US-09-352-616A-114 (1-241)
QY 1 GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAG 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
33 SerileaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52
QY 61 TTTGTCAACGTGGGCTACTTCTCATCGACGCCGGTGTGGTCTTTTGTCTTGGTTTC 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
53 PheValaenValGlyTyPheLeuIleAlaAaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCT 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
73 LeuGlyCysTyGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheile 92
QY 181 CTCCTCTCATCTTTCATTGCTGAGGTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValValAlaLeuValThrThrThr 112
QY 241 ATGGCTGAGCACTTCCCGACGTTTGGTGTAGTGCCTGCCATCAAGAAG 288
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
113 MetAlaGluHisPheLeuThrLeuValValProAlaIleLysLys 128

RESULT 6
US-09-439-313-114
; Sequence 114, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-439-313-114

Alignment Scores:
Pred. No.: 9.61e-46 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 2 Gaps: 0

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Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 8

US-09-232-149A-114

; Sequence 114, Application US/09232149A

; Patent No. 6465611

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427C6

; CURRENT APPLICATION NUMBER: US/09/232,149A

; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-232-149A-114

Alignment Scores:

Pred. No.:	9,61e-46	Length:	241
Score:	453.00	Matches:	93
Percent Similarity:	97.9%	Conservative:	1
Best Local Similarity:	96.9%	Mismatches:	2
Query Match:	80.3%	Indels:	0
DB:	2	Gaps:	0

US-10-079-954-1 (1-297) x US-09-232-149A-114 (1-241)

QY	1	GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTGCAGTGCATGCAG	60
Db	33	SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln	52
QY	61	TTTGTCACGTGGGCTACTCTCTCATCGACCGCGGTGGTCTTGGCTCTTGGTTTC	120
Db	53	PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe	72
QY	121	CTGGCTGCTATGCTGAAGACTGAGACAGTGTGCGCTCGTGCACGTTCTTCTTCATC	180
Db	73	LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe	92
QY	181	CTCTCTCATCTTCATTTGCTGAGTTGCAGTGTGCTGGTGGCTGGTGTACACATA	240
Db	93	LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr	112
QY	241	ATGGCTGAGCACTTCCCGACGTTGCTGGTAGTCGCTGCCATCAAGAAG	288
Db	113	MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys	128

RESULT 9

US-09-159-812-114

; Sequence 114, Application US/09159812A

; Patent No. 6613872

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF

; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.428C5

; CURRENT APPLICATION NUMBER: US/09/159,812A

; CURRENT FILING DATE: 1998-09-23

; NUMBER OF SEQ ID NOS: 306

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-159-812-114

Alignment Scores:

Pred. No.:	9,61e-46	Length:	241
Score:	453.00	Matches:	93
Percent Similarity:	97.9%	Conservative:	1
Best Local Similarity:	96.9%	Mismatches:	2
Query Match:	80.3%	Indels:	0
DB:	2	Gaps:	0

US-10-079-954-1 (1-297) x US-09-159-812-114 (1-241)

QY	1	GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTGCAGTGCATGCAG	60
Db	33	SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln	52
QY	61	TTTGTCACGTGGGCTACTCTCTCATCGACCGCGGTGGTCTTGGCTCTTGGTTTC	120
Db	53	PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe	72
QY	121	CTGGCTGCTATGCTGAAGACTGAGACAGTGTGCGCTCGTGCAGTGTCTTCTTCATC	180
Db	73	LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe	92
QY	181	CTCTCTCATCTTCATTTGCTGAGTTGCAGTGTGCTGGTGGCTGGTGTACACATA	240
Db	93	LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr	112
QY	241	ATGGCTGAGCACTTCCCGACGTTGCTGGTAGTCGCTGCCATCAAGAAG	288
Db	113	MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys	128

RESULT 10

US-09-636-215-114

; Sequence 114, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-636-215-114

Alignment Scores:

Pred. No.:	9,61e-46	Length:	241
Score:	453.00	Matches:	93
Percent Similarity:	97.9%	Conservative:	1
Best Local Similarity:	96.9%	Mismatches:	2
Query Match:	80.3%	Indels:	0
DB:	2	Gaps:	0

Best Local Similarity: 96.9%
 Query Match: 80.3%
 DB: 2
 Mismatches: 2
 Indels: 0
 Gaps: 0

US-10-079-954-1 (1-297) x US-09-759-143-114 (1-241)

Qy	1	GCAATCGATGGGCGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAG	60
		:::	
Db	33	SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln	52
Qy	61	TTTGTCAACGTGGGCTACTTCCTCATCCAGCGCGTGTGGTCTTTGCTCTTGGTTTC	120
Db	53	PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe	72
Qy	121	CTGGGCTGCTATGGTGTAAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCTTCATC	180
Db	73	LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe	92
Qy	181	CTCCTCTCATCTTCATTTGCTGAGGTTGCAGCTGTGTGGTGGCTTGGTGTACACCATATA	240
Db	93	LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValThrThr	112
Qy	241	ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAAG	288
Db	113	MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys	128

Search completed: March 23, 2006, 12:49:01
 Job time : 30.1452 secs

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:40:14 ; Search time 3.60161 Seconds
(without alignments)
1394.518 Million cell updates/sec

Title: US-10-079-954-2
Perfect score: 502
Sequence: 1 agccagcgaacgagcagggg.....tttacctcaagtgtgttaa 261

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs/ABSSWEB_spool/US10079954/runat_23032006_102931_1829/app_query.fasta_1
-DB=PIR -QMT=FASTA -SUFFIX=rpr -MINMATCH=0.1 -DOOPCL=0 -IDOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10079954 -CGEN 1 1 77 @runat_23032006_102931_1829 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCk=100 -LONGLOG -DRV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.5	14.4	342	2	JC7110 brain-specific mem
2	71	14.1	586	2	B70503 probable pyrG prot
3	69	13.7	424	2	F71087 hypothetical prote
4	69	13.7	1700	2	S08167 Balbiani ring 3 pr
5	67.5	13.4	1515	2	S51824 myosin heavy chain
6	66.5	13.2	770	2	S80676 cellobiose oxidase
7	66.5	13.2	1057	1	ORTR atrial natriuretic
8	66.5	13.2	1057	2	I55319 guanylyl cyclase A
9	66.5	13.2	1057	2	I57963 natriuretic peptid
10	66	13.1	372	1	HOECNS hydroxylase (EC 1.
11	66	13.1	372	2	D85632 hydroxylase-1 smal
12	66	13.1	372	2	H90769 hydroxylase-1 smal
13	66	13.1	1182	2	T30189 myelin transcripti
14	66	13.1	1187	2	T46637 transcription fact

15	66	13.1	1188	2	T46608
16	66	13.1	1390	1	TVHUME
17	65.5	13.0	201	2	H84990
18	65.5	13.0	496	2	A54770
19	65.5	13.0	1534	2	S59604
20	65	12.9	430	2	T14422
21	65	12.9	430	2	T14536
22	65	12.9	455	2	A61545
23	65	12.9	725	2	A45033
24	65	12.9	858	2	S68227
25	64.5	12.8	788	2	G81294
26	64.5	12.8	938	2	G70472
27	64	12.7	350	2	AG1407
28	64	12.7	350	2	AG1783
29	64	12.7	627	4	A40201
30	64	12.7	647	1	S42939
31	64	12.7	811	2	S08579
32	63.5	12.6	104	2	AC2099
33	63.5	12.6	309	2	A11810
34	63.5	12.6	360	2	T04829
35	63.5	12.6	364	1	S77360
36	63.5	12.6	372	2	JC2556
37	63.5	12.6	640	2	S49932
38	63.5	12.6	768	2	D97626
39	63.5	12.6	772	2	D96504
40	63.5	12.6	900	2	T07717
41	63.5	12.6	990	2	T03784
42	63.5	12.6	1057	1	OYMSAR
43	63.5	12.6	1902	2	C97702
44	63.5	12.6	2318	2	S45306
45	63.5	12.6	4660	2	T42737

ALIGNMENTS

RESULT 1

JC7110
brain-specific membrane anchor protein - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: JC7110
R:Eison, G.C.A.; de Coignac, A.B.; Aubry, J.P.; Delneste, Y.; Magistrelli, G.; Holzwarth
Biochem. Biophys. Res. Commun. 264, 55-62, 1999
A:Title: BSMAP, a novel protein expressed specifically in the brain whose gene is local
A:Reference number: JC7110; MUID:99458621; PMID:10527841
A:Accession: JC7110
A:Molecule type: mRNA
A:Residues: 1-342 <EUS>
A:Cross-references: UNIPROT:Q9UK28; UNIPARC:UPI0000034024; GB:AF186264; NID:96003653; PI:
C:Genetics:
A:Gene: bsmap
A:Map position: 19p12
C:Superfamily: human brain-specific membrane anchor protein
C:Keywords: brain; glycoprotein; membrane bound; transmembrane protein

Alignment Scores:				
Pred. No.:	6.99	Length:	342	
Score:	72.50	Matches:	24	
Percent Similarity:	45.0%	Conservative:	12	
Best Local Similarity:	30.0%	Mismatches:	29	
Query Match:	14.4%	Indels:	15	
DB:	2	Gaps:	4	

US-10-079-954-2 (1-261) x JC7110 (1-342)

Qy	22	GACATAGAGTGGTGTCTATGCTTGTGAGAGAGAAACACTTTCGAGTGCAGAACCCA	81
Db	69	AspArgAlaValLeuIleSerAlaCysGluArg	84
Qy	82	AGGAGGTGCAATGCG	114
Db	85	SerIleCysArgPheValAlaArgSerLysProAsnAlaThrGlnGluCysGlu	104

zinc finger protei
hepatocyte growth
SOS ribosomal prot
N-acetylglucosamin
DNA (cytosine-5)-
S-locus-specific g
S-locus-specific g
plasmin (EC 3.4.21
myelin transcripti
ubiquitin thiolest
hypothetical prote
hypothetical prote
sorbitol dehydroge
sorbitol dehydroge
artifect-warnin g
malate dehydrogena
hypothetical prote
hypothetical prote
DHNA phythltransfe
hypothetical prote
cbiD protein - Syn
alpha-1-microglobu
MST30 protein - ye
hypothetical prote
protein F9C16.25 [
probable ABC-type
probable receptor
atrial natriuretic
cell surface anti g
notch 3 protein -
gp330 protein prec

C; Keywords: oxidoreductase
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-770/Product: cellobiose oxidase #status predicted <MAT>

Alignment Scores:

Pred. No.:	33.6	Length:	770
Score:	66.50	Matches:	27
Percent Similarity:	39.3%	Conservative:	8
Best Local Similarity:	30.3%	Mismatches:	32
Query Match:	13.2%	Indels:	22
DB:	2	Gaps:	4

US-10-079-954-2 (1-261) x S60676 (1-770)

QY	223	CCAGGAGAAACCGCTTCTCTCGCTGGTGGTC-----TCTCCATCGCTGCACCAACCAG	170
Db	603	ProGlySerLeuArgGluLeuAlaValGlnArgGluProAspLeuHisAspHis	622
QY	169	CGAGACACCTGTTCCGACACCAACCAAAACCTGGAAATATTTTCACGGCGGCTATAACGC	110
Db	623	Arg-ValProLeuTyrGlyHisProValAlaTyrAlaHisArgHis-----ArgSerAl	640
QY	109	AGTATGCGCTGTGCTCACTTGCACCTCCTTGGTGGTCTCG-----	73
Db	640	aleuArgGlyThrValLeuThrProPrtProLeuValAsnProValAspLysThrValle	660
QY	72	-----GCATCGAAAGTGTCTCTCT-----CTCACAGCATC	41
Db	660	uLeuGlnAlaLeuHisAspValValSerAsnIleGlySerIleProGlyLeuThrMetIl	680
QY	40	GACACCACTCTATTGTCAACCTC 16	
Db	680	eThrProAspValThrGlnThrLeu 688	

RESULT 7
OXYTRK

atrial natriuretic peptide receptor A precursor - rat
N; Alternate names: guanylate cyclase A, membrane-bound
N; Contains: guanylate cyclase (EC 4.6.1.2) A
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C; Accession: S03348; A13303
R; R; Chinkers, M.; Garbers, D.L.; Chang, M.S.; Lowe, D.G.; Chin, H.; Goeddel, D.V.; Schulz, Nature 338, 78-83, 1989
A; Title: A membrane form of guanylate cyclase is an atrial natriuretic peptide receptor.
A; Reference number: S03348; MUID:89143770; PMID:2563900
A; Accession: S03348
A; Molecule type: mRNA
A; Residues: 1-1057 <CHI>
A; Cross-references: UNIPROT:P18910; UNIPARC:UPI000012583F; EMBL:X14773; NID:G56339; PIDN:AAA41202.1; PID:5
R; Duda, T.; Goraczniak, R.M.; Sharma, R.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 7882-7886, 1991
A; Title: Site-directed mutational analysis of a membrane guanylate cyclase cDNA reveals t
A; Reference number: A41303; MUID:91352095; PMID:1679239
A; Accession: A41303
A; Molecule type: mRNA
A; Residues: 1-365, 'H', 367-391, 'P', 393-1057 <DUD>
A; Cross-references: UNIPARC:UPI000017096E; GB:M74535; NID:9204269; PIDN:AAA41202.1; PID:5
C; Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homol
C; Keywords: ATP; carbon-oxygen lyase; cGMP biosynthesis; glycoprotein; hormone receptor;
F; 1-28/Domain: signal sequence #status predicted <SIG>
F; 29-1057/Product: atrial natriuretic peptide receptor #status predicted <MAT>
F; 29-469/Domain: extracellular #status predicted <EXT>
F; 109-449/Domain: natriuretic peptide-binding domain homology <NPB>
F; 470-490/Domain: transmembrane #status predicted <TM>
F; 491-1057/Domain: intracellular #status predicted <INT>
F; 522-804/Domain: protein kinase homology <KIN>
F; 824-1051/Domain: guanylate cyclase catalytic domain homology <GCC>
F; 41, 208, 334, 375, 382, 423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

Pred. No.:	33.6	Length:	1057
Score:	66.50	Matches:	27

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:33:09 ; Search time 16.5581 Seconds
(without alignments)
2224.208 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 502

Sequence: 1 agccaggaacgacgagg.....tttacctcaagtgtgttaa 261

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs8/ABSSWEB/spool/US10079954/runat_23032006_102929_1793/app_query.fasta_1
-DB=UniProt -QFMT=fastcan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=ext -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs802p
-USER=US10079954 @CGN 1.1.580 @runat_23032006_102929_1793 -NCPU=6 -ICPU=3
-NO_WMAP -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	482	96.0	179	2	Q9BVD7 HUMAN	Q9bvd7 homo sapien
2	478	95.2	224	2	O15227 HUMAN	O15227 homo sapien
3	205	40.8	154	2	Q9CWP4 MOUSE	Q9cwp4 mus musculus
4	110.5	22.0	176	2	Q9QUL5 MOUSE	Q9qul5 mus musculus
5	97.5	19.4	158	1	GML HUMAN	G99445 homo sapien
6	96.5	19.2	176	2	Q9DAP4 MOUSE	Q9dap4 mus musculus
7	81	16.1	310	2	Q7S5T7 NEUTR	Q7s5t7 neutropora
8	80	15.9	583	2	Q740ES MYCPA	Q740es mycobacteri
c 9	78.5	15.6	201	2	Q4S211 TETNG	Q4s211 tetraodon n
c 10	77.5	15.4	472	2	Q978V2 THEVO	Q978v2 thermoplasm
c 11	77.5	15.4	493	2	Q6KZ09 PICTO	Q6kz09 picophilus
c 12	76	15.1	251	2	Q4J5Z9 AZOVI	Q4j5z9 azotobacter
c 13	76	15.1	1475	2	Q7N7Y2 PHOLL	Q7n7y2 photorhabdu
c 14	73	14.5	317	2	Q6D9G3 ERWCT	Q6d9g3 erwinia car
c 15	73	14.5	326	2	Q7X844 ORISA	Q7x844 oryza sativ
16	73	14.5	345	2	Q4SC28 TETNG	Q4sc28 tetraodon n

17	72.5	14.4	342	1	BSMAP HUMAN	Q9uk28 homo sapien
18	72	14.3	554	2	O57473 XENLA	O57473 xenopus lae
c 19	71.5	14.2	350	2	O5A300 CANAL	O5a300 candida alb
c 20	71.5	14.2	589	2	Q8NDX2 HUMAN	Q8ndx2 homo sapien
21	71.5	14.2	1474	2	Q8GFP9 PHOLU	Q8gfp9 photorhabdu
22	71	14.1	449	2	Q6YTJ0 ORISA	Q6ytj0 oryza sativ
23	71	14.1	586	1	PYRG MYCTU	P0a5u2 mycobacteri
24	71	14.1	586	1	PYRG MYCTU	P0a5u2 mycobacteri
25	71	14.1	1145	2	O6C7Y9 VARLI	O6c7y9 varrowia li
26	70.5	14.0	97	2	O86SR0 HUMAN	O86sr0 homo sapien
27	70.5	14.0	131	2	Q8NSJ9 HUMAN	Q8nsj9 homo sapien
28	70.5	14.0	336	2	Q873P9 MUCMU	Q873p9 mucor muced
c 29	70.5	14.0	485	2	Q9HLC1 THEAC	Q9hlc1 thermoplasm
c 30	70	13.9	120	2	Q4T8C6 TETNG	Q4t8c6 tetraodon n
c 31	70	13.9	369	2	Q4LZG8 BURK	Q4lzg8 burkholderi
c 32	70	13.9	503	2	Q9LSC6 ARATH	Q9lsc6 arabidopsis
c 33	70	13.9	534	2	Q4WG10 ASPFU	Q4wg10 aspergillus
34	70	13.9	1704	2	Q94446 IDIPT	Q94446 chironomus
c 35	69.5	13.8	294	2	Q53VX1 THETH	Q53vx1 thermus the
c 36	69.5	13.8	411	2	Q50Q35 ENTHI	Q50q35 entamoeba h
c 37	69	13.7	309	2	Q7F1K9 ORISA	Q7f1k9 oryza sativ
c 38	69	13.7	375	1	MBHS CITFR	O46045 citrobacter
c 39	69	13.7	424	1	Y963 PYRHO	O58701 pyrococcus
c 40	69	13.7	500	2	Q891J6 BRAJA	Q891j6 bradyrhizob
c 41	69	13.7	763	1	RINI MOUSE	Q921q7 mus musculu
c 42	69	13.7	1003	2	Q6AUV7 ORISA	Q6auv7 oryza sativ
43	69	13.7	1700	1	BAR3 CHITE	Q03376 chironomus
44	68.5	13.6	139	1	LY6H MOUSE	Q9wuc3 mus musculu
45	68.5	13.6	139	2	Q544M1 MOUSE	Q544m1 mus musculu

ALIGNMENTS

RESULT 1
Q9BVD7 HUMAN
ID Q9BVD7 HUMAN PRELIMINARY; PRT; 179 AA.
AC Q9BVD7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LY6K protein (Fragment).
GN Name=LY6K;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoig L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.B.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.

QY 1 AGCCAGCGAACGGACGAGGGTGACAAATAGAGTGTGGTGTGCTCAT

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., King B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vercardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamuro T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL [7]
RN NUCLEOTIDE SEQUENCE.
RC TISSUS=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Stalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC TISSUS=Testis;
RA Straubeberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK010485; BAB26976.1; -; mRNA.
DR EMBL; BC049723; AAH49723.1; -; mRNA.
DR Ensembl; ENSMUSG0000044678; Mus musculus.
DR MGI; MGI:1923736; Ly6k.
DR InterPro; IPR001526; LY6 UPAR.
DR InterPro; IPR008197; WAP.
DR PRINTS; PR00003; 4DISULPHORE.
DR SMART; SM00134; LU; 1.
RW Hypothetical protein.
SQ SEQUENCE 154 AA; 17134 MW; F756PBB2B3B400C6 CRC64;
Alignment Scores:
Pred. No.: 2.54e-14 Length: 154
Score: 205.00 Matches: 33
Percent Similarity: 57.6% Conservative: 16
Best Local Similarity: 38.8% Mismatches: 30
Query Match: 40.8% Indels: 6
DB: 2 Gaps: 1
US-10-079-954-2 (1-261) x Q9CWP4_MOUSE (1-154)
Qy 25 AATAGAGTGTGTCTATGCTGTGAGAGAGAAACACTTTCGAGTCCGACCAAGG 84
Db 19 AShAlaLeuThrCysHisValCysGluAlaGlnAenSerTyrAlaCysSerAsnProSer 38
Qy 85 AGTGCCTAAATGGACAGAGCCATCTCGTTATAGCGCCGCTGAAATATTTCCACGTTT 144
Db 39 GlnCysProGlyGluLysLysPheCysLeuLeuAlaValThrArgIlePheGluArgPhe 58
Qy 145 TTCTATGTTCTGCAACAGGTCTCGCTGTGTGTGTCGCGC-----ATG 186
Db 59 PheTyrValSerLysGlnCysThrArgArgCysProThrProValValSerProProSer 78
Qy 187 GAGAGACCCCAAGCAGAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCTTTTAC 246
Db 79 ThrAsnProSerGluProLysGluPheLeuIleGluLysProMetProPheLeuPhe 98
Qy 247 CTCAGCTGTGTATAA 261
Db 99 TyrLysCysGln 103
RESULT 4
Q9CUL5_MOUSE
ID Q9CUL5_MOUSE PRELIMINARY; PRT; 176 AA.
AC Q9CUL5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE HemT-3 protein.
GN Name=HemT;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

```
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=99250249; PubMed=10231568; DOI=10.1016/S0378-1119(99)00099-2;
RA Xue H., O'Neill D., Morrow J., Bank A.;
RT "A novel mouse gene, Hemt, encoding an hematopoietic cell-specific
RL transcript.";
RL Gene 231:49-58(1999).
RN NUCLEOTIDE SEQUENCE.
RA Xue H., O'Neill D., Wang X., Wolgemuth D., Bank A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ242831; CAB57316.1; -; mRNA.
DR EMBL; AJ242830; CAB57315.1; -; Genomic_DNA.
DR InterPro; IPR001526; LY6_UPAR.
DR SMART; SM001134; LU; 1.
SQ SEQUENCE 176 AA; 20170 MW; 85584EE92EDE275E CRC64;

Alignment Scores:
Pred. No.: 0.00176 Length: 176
Score: 110.50 Matches: 24
Percent Similarity: 45.5% Conservative: 16
Best Local Similarity: 27.3% Mismatches: 39
Query Match: 22.0% Indels: 9
Db: 2 Gaps: 3

US-10-079-954-2 (1-261) x Q9QUL5_MOUSE (1-176)
QY 22 GACATATAGAGT-----TGG-----TGCTGCTGTGTGAGAGAGAA 57
Db 36 AspAsnAlaIleGluProArgTrpThrProGlnMetArgCysHisSerCysGlnGluHis 55
QY 58 AACACTTTCGATGCCAGAACCCAGGAGTGCAAATGACAGAGCCCATCTCGTGTATA 117
Db 56 AanthrPheTyrcysProHisIleHisTyrcysAspMetAspIleArgArgCysLeuThr 75
QY 118 GGGCGCGTGAAATATTTCCAGGTTTTCATGTTCCACAGGTGCTCCGCTGGTGT 177
Db 76 ValAlaIleArgValAsnIleArgLeuLeuTyValLeuLysAspCysThrLysAspCys 95
QY 178 GCAGCGATGAGAGAGACCCCAAG---CCAGAGGAGAGCGGTTTCTCTCGAAGAGCCCATG 234
Db 96 ThrPheIleTyArgGluHisValProGlnGluLeuProArgValLeuLysAspValLys 115
QY 235 CCCTCTTTTACCTCAAGTGTGT 258
Db 116 AsnPheTyrcysValMetCysCys 123

RESULT 5
GML_HUMAN
ID - GML_HUMAN STANDARD; PRT; 158 AA.
AC Q99445; O00686; O00731;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glycosyl-phosphatidylinositol-anchored molecule-like protein
DE precursor.
GN Name=GML; Synonyms=LY6DL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=97088635; PubMed=8934543;
RA Furuhashi T., Tokino T., Urano T., Nakamura Y.;
RT "Isolation of a novel GPI-anchored gene specifically regulated by p53;
RL correlation between its expression and anti-cancer drug sensitivity.";
RN Oncogene 13:1965-1970(1996).
RP NUCLEOTIDE SEQUENCE.
```

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RX MEDLINE=97312709; PubMed=9169150; DOI=10.1006/geno.1997.4680;
RA Kimura Y., Furuhashi T., Urano T., Hirata K., Nakamura Y., Tokino T.;
RT "Genomic structure and chromosomal localization of GML (GPI-anchored
RL molecule-like protein), a gene induced by p53.";
RN Genomics 41:477-480(1997).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC -1- FUNCTION: May play a role in the apoptotic pathway or cell-cycle
CC regulation induced by p53 after DNA damage.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -1- INDUCTION: By p53.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; D84290; BAA12300.1; -; mRNA.
CC EMBL; AB000381; BAA19961.1; -; Genomic_DNA.
CC EMBL; BC074930; AAH74930.1; -; mRNA.
CC Ensembl; ENSG00000104499; Homo sapiens.
CC HGNC; HGNC:4375; GML.
CC MIM; 602370; -.
CC GO; GO:0019898; C:extrinsic to membrane; TAS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0006915; P:apoptosis; TAS.
CC GO; GO:0006977; P:DNA damage response, signal transduction by...; TAS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
CC GO; GO:0000074; P:regulation of cell cycle; TAS.
CC InterPro; IPR001526; LY6_UPAR.
CC SMART; SM00134; LU; 1.
CC PROSITE; PS00983; LY6_UPAR; 1.
KW GPI-anchor; Lipoprotein; Membrane; Polymorphism; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 158 Glycosyl-phosphatidylinositol-anchored
FT molecule-like protein.
FT DOMAIN 29 134 UPAR/Ly6.
FT DISULFID 31 55 By similarity.
FT DISULFID 34 42 By similarity.
FT DISULFID 48 73 By similarity.
FT DISULFID 77 104 By similarity.
FT DISULFID 105 110 By similarity.
FT VARIANT 54 54 R -> C (in dbSNP:3764795).
FT /FTID=VAR_020174.
SQ SEQUENCE 158 AA; 17730 MW; 21D7F23D33DBB3B2 CRC64;

Alignment Scores:
Pred. No.: 0.0534 Length: 158
Score: 97.50 Matches: 23
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Percent Similarity: 46.2% Conservatives: 13
 Best Local Similarity: 29.5% Mismatches: 35
 Query Match: 19.4% Indels: 7
 DB: 1 Gaps: 2

US-10-079-954-2 (1-261) x GML_HUMAN (1-158)

QY 37 TGTCATGCTTGTGAGAGAAACACTTTTCGAGTGCAGACCCCAAGAGGTGCAATGG 96
 Db CysHisAspCysAlaValIleAsnAspPheAsnCysProAsnIleArgValCysProTyr 50
 QY 97 ACAGAGCCATACCTGCTGTATAGCGCCGCTGAAATATTTCCACGTTTTCATGGTTCG 156
 Db HisIleArgA-gCysMetThrIleSerIleArgIleAsnSerArggIleuLeuValTyr 70
 QY 157 AACAGGTGCTCGCTGGTGTG-----GCAGCGATGAGACCCCAAGCCAGAG 204
 Db LysAsnCysThrAsnAsnCysThrPheValTyrAlaIleGluInProGluAlaPro 90
 QY 205 GAGAGCGGTTTCTCTCGAGAGCCCGCCCTTTTACCTCAAGTGTGT 258
 Db GlyLysIlePhe-----LysThrAsnSerPheTyrTrpValCysCys 105

RESULT 6

Q9DAP4_MOUSE
 ID Q9DAP4_MOUSE PRELIMINARY; PRT; 176 AA.
 AC Q9DAP4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:1700003p22 product:hematopoietic cell transcript 1,
 DE full insert sequence.
 GN Name=Hemtl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
 RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:695-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;

RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:11617-1630(2000).
 [5]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:11757-1771(2000).
 [6]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima T., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK005659; BAB24171.1; -; mRNA.
 DR MGI; MGI:1341831; Hemt1.
 DR InterPro; IPR001526; LY6_UPAR.
 DR SMART; SM00134; LU; 1.
 DR SEQUENCE 176 AA; 19890 MW; 8D595E54A7A5C3A6 CRC64;
 Alignment Scores:
 Pred. No.: 0.0707 Length: 176
 Score: 96.50 Matches: 23
 Percent Similarity: 40.9% Conservatives: 13
 Best Local Similarity: 26.1% Mismatches: 43
 Query Match: 19.2% Indels: 9
 DB: 2 Gaps: 3

US-10-079-954-2 (1-261) x Q9DAP4_MOUSE (1-176)

QY 22 GACAATAGAGT-----TGG-----TGTCATGCTTGTGAGAGAGAA 57
 Db AspAsnAlaIleGluProArgTrpSerProValLeuThrCysHisLysCysTyrIleSer 55
 QY 58 AACACTTTCGAGTCCAGACCCAGGAGGTCGAATGGACAGACCATCTCGGTATA 117
 Db ValSerPheArgValAsnIleArgLeuTyrValLeuLysAspCysThrLysAspCys 95
 QY 118 GCGGCGGTGAAATATTTCCACGTTTTTTCATGCTTCGCAACAGGTGCTCGGTGTGT 177
 Db ValSerPheArgValAsnIleArgLeuTyrValLeuLysAspCysThrLysAspCys 95
 QY 178 GCAGCGATGGAGAGACCAAG---CCAGAGGAGAGCGGTTTCTCTGGAGAGCCCATG 234

Qy	121	GC	CGTGGAATAATTTCCAGCGTTTTTCATGTTCCGAC	159
		:::		
Db	196	Asp	ThrGluPhePheProAlaAspGluValMetAsn	208
		:::		
RESULT 8				
Q740E5	MYCPA			
ID	Q740E5_MYCPA	PRELIMINARY;	PRT;	583 AA.
AC	Q740E5;			
DT	05-JUL-2004	(TReMBLrel. 27, Created)		
DT	05-JUL-2004	(TReMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TReMBLrel. 27, Last annotation update)		
DE	Pyrg.			
GN	Name=pyrg; OrderedLocusNames=MAP1406;			
OS	Mycobacterium paratuberculosis.			
OS	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium;			
OC	Mycobacterium avium complex (MAC).			
NCBI_TaxID=1770;				
ON	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=k10;			
RL	Li L., Barnantine J., Zhang Q., Anonsin A., Alt D., Kapur V.			
RL	Submitted (SEP-2003) to the EMBL/Genbank/DBS databases.			
EMBL;	AS017232.1; AA03723.1; -; Genomic DNA.			
GO;	GO:0003883; F-CTP synthase activity; IEA.			
DR	GO:0016874; F-ligase activity; IEA.			
DR	GO:0004541; P-glutamine metabolism; IEA.			
DR	GO:0006221; P-pyrimidine nucleotide biosynthesis; IEA.			
DR	InterPro; IPR000991; GATase_1.			
DR	InterPro; IPR004468; Pyrg_synth.			
DR	Pfam; PF06418; CTP synth_N; 1.			
DR	Pfam; PF00117; GATase; 1.			
DR	TIGRFAMS; TIGR00337; Pyrg; 1.			
DR	PROSITE; PS00442; GATASE_TYPE_I; 1.			
DR	Complete proteome.			
SK	SEQUENCE 583 AA; 63142 MW; 8BCA048A64D906B9			CRC64;
Alignment Scores:				
Pred. No.:	6.62	Length:	583	
Score:	80.00	Matches:	21	
Percent Similarity:	43.7%	Conservative:	10	
Best Local Similarity:	29.6%	Mismatches:	30	
Query Match:	15.9%	Indels:	10	
DB:	2	Gaps:	1	
US-10-079-954-2 (1-261) x Q740E5_MYCPA (1-583)				
Qy	66	CG	AGTCCGCAACCCACGAG--	-----
Db	294	Arg	ValHisGluProHisGluThrValArgIleAlaLeuValGlyLysTyr	7r
Qy	96	GAC	GAGCCATACCTCGGTTATAGCGCGCTGAAATATTTCACGTTTTT	
Db	314	Ser	AspAlaTyrLeuSerValThrGluAlaLeuArgAlaGlyGlyPhePhe	
Qy	156	CAC	AGGTGCTCGCTGGTTGTGCAGCATGGAGACCCAGCCAGGAGNA	
	:::	:::		
Db	334	Lys	ValGluMetValTyrValAlaSerAspCysGluSerAlaSerGly	
	:::	:::		
Qy	216	TC	CTCTGGGAAGCCCATGCCCTCTCTTTACCT	248
	:::	:::		
Db	354	Ala	GlyGluValHisGlyValLeuIlePro	364
	:::	:::		
RESULT 9				
Q4S211	TETNG			
ID	Q4S211_TETNG	PRELIMINARY;	PRT;	201 AA.
AC	Q4S211;			
DT	13-SEP-2005	(TReMBLrel. 31, Created)		
DT	13-SEP-2005	(TReMBLrel. 31, Last sequence update)		
DT	13-SEP-2005	(TReMBLrel. 31, Last annotation update)		
DE	Chromosome 17 SCAFL4760, whole genome shotgun sequence.			
GN	ORFNAMES=GSTENG002506001;			
OS	Tetradon nigroviridis (Green puffer).			

Search completed: March 23, 2006, 12:45:56
Job time : 87.7903 secs

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:29:14 ; Search time 19.271 Seconds

(without alignments)
1190.162 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 502

Sequence: 1 agccagcgaacgacgaggg.....tttacctcaagtgtgttaa 261

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs/ABSSWEB pool/US1007954/runat_23032006_102927_1781/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SURFIX=rag -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US1007954 @CGN 1.1 476 @runat_23032006_102927_1781 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -BSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Geneseq21980s:*
2: Geneseq21980s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	482	96.0	162	5 ABP42766	Human ova
2	482	96.0	165	5 ABG61944	Prostate
3	482	96.0	165	6 ABUS6446	Lung canc
4	482	96.0	165	7 ADN39436	Cancer/an
5	482	96.0	166	8 ADU06395	Novel bro
6	482	96.0	223	2 AAU81754	Human Fan
7	482	96.0	223	6 ABR48226	Human bla
8	482	96.0	223	6 ABUS6671	Lung canc
9	482	96.0	223	7 ADN39022	Cancer/an

10	482	96.0	248	7 ADF60487	Human con
11	482	96.0	248	8 ADS12252	Human the
12	375	74.7	171	7 ADF59395	Human pol
13	371.5	74.0	162	8 ADS11037	Human the
14	205	40.8	154	5 ADI17070	Murine NO
15	97.5	19.4	158	2 AAU36523	GPI ancho
16	81	16.1	240	8 ADN21057	Bacterial
17	80	15.9	583	6 ABU33887	Protein e
18	78.5	15.6	342	7 ADA45175	Human pol
19	77	15.3	106	4 AAU62645	Propionib
20	77	15.3	106	6 ABMS9164	Propionib
21	76	15.1	136	6 ABR41162	Human DiT
22	76	15.1	1476	6 ABM70222	Photothab
23	75	14.9	159	7 ABO79796	Pseudomon
24	75	14.9	636	6 ABUL7389	Protein e
25	73	14.5	136	7 ABO71446	Pseudomon
26	72.5	14.4	286	7 ADG14985	Human SEC
27	72.5	14.4	309	8 ADJ66975	Human sec
28	72.5	14.4	342	2 AAY16785	Brain spe
29	72.5	14.4	342	3 AAB00163	Human pro
30	72.5	14.4	353	4 AAM25782	Hepatitis
31	72.5	14.4	3011	2 AAR95021	Human TRI
32	71.5	14.2	588	6 AAE32079	Human tra
33	71.5	14.2	589	5 AAU99329	Human tra
34	71.5	14.2	589	6 AAO30994	Human tra
35	71.5	14.2	589	7 ADD01392	Human TCH
36	71.5	14.2	589	7 ADG88329	Human tra
37	71.5	14.2	589	8 ADR10021	Human pro
38	71.5	14.2	1474	8 ADP18622	Photothab
39	71.5	14.2	1474	8 ADR21525	Photothab
40	71	14.1	543	6 ABUS4884	Protein e
41	71	14.1	586	6 ABUS36674	Protein e
42	70.5	14.0	97	3 AAY87278	Human sig
43	70.5	14.0	97	3 AAB18912	A novel p
44	70.5	14.0	97	4 AAU29257	Human PRO
45	70.5	14.0	97	6 ABUS8633	Human PRO

ALIGNMENTS

RESULT 1

ABP42766
ID ABP42766 standard; protein; 162 AA.

XX ABP42766;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HOVKE66, SEQ ID NO:3898.

Human; ovarian antigen; ovary; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
inflammatory condition; immune disorder; blood disorder;
cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytostatic; immunomodulatory; neuroprotective;
antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX

PI Birse CE, Rosen CA;
 XX WPI; 2002-147878/19.
 DR N-PSDB; ABQ55843.
 XX
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 XX Claim 11; SEQ ID NO 3898; 2922pp; English.
 PS
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 162 AA;

Alignment Scores:
 Pred. No.: 1.69e-47 Length: 162
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 5 Gaps: 0

US-10-079-954-2 (1-261) x ABP42766 (1-162)

QY 1 AGCCAGCAAGGAGGAGGACATAGAGTGTGTCTCATGCTTGTGAGAGAAAC 60
 Db 28 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 47
 QY 61 ACTTTCGAGTGCAGAACCCCAAGGAGGTGCAATAGCAGAGCCATCTGCGTTATAGCG 120
 Db 48 ThrPheGluCysGlnAsnProArgArgCysIleTrpThrGluProTrpCysValIleAla 67
 QY 121 GCGGTGAAATATTTCACAGTCTTTTCATGTTTCGCAACAGGTGCTCGGTGTGCA 180
 Db 68 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 87
 QY 181 GCGATGAGAGACCAACGACGAGAGAGCGGTTCTCTCGAAGAGCCCATCCCTTC 240
 Db 88 AlaMetGluArgProGlyProGluGlyArgPheLeuLeuGluGluProMetProPhe 107
 QY 241 TTTTACCTCAAGTGTGTGAAA 261
 Db 108 PheTyrLeuLysCysCysLys 114

RESULT 2

ABG61944
 ID ABG61944 standard; protein; 165 AA.

XX AC ABG61944;

XX 15-AUG-2002 (first entry)

XX Prostate cancer-associated protein #145.

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.

XX Mammalia.

XX WO200230268-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-US032045.

XX 13-OCT-2000; 2000US-00687576.

XX 08-DEC-2000; 2000US-00733288.

XX 08-DEC-2000; 2000US-00733742.

XX 24-JAN-2001; 2001US-0263957P.

XX 16-MAR-2001; 2001US-0276791P.

XX 16-MAR-2001; 2001US-0276888P.

XX 06-APR-2001; 2001US-0281922P.

XX 24-APR-2001; 2001US-0286214P.

XX 30-APR-2001; 2001US-00847046.

XX 04-MAY-2001; 2001US-0288589P.

XX (SO5B-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

XX WPI; 2002-471335/50.

XX N-PSDB; ABK92263.

XX Detecting a prostate cancer-associated transcript in a cell in a patient,

XX useful for diagnosing prostate cancer (PC) or screening modulators of PC,

XX by determining if prostate cancer-associated genes are expressed in a

XX prostate tissue.

XX Claim 27; Page 427; 436pp; English.

XX The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

XX ABG61800-ABG61944 represent prostate cancer-associated proteins

XX Sequence 165 AA;

Alignment Scores:
 Pred. No.: 1.7e-47 Length: 165

Score: 482.00 Matches: 83

Percent Similarity: 96.6% Conservative: 1

Best Local Similarity: 95.4% Mismatches: 3

Query Match: 96.0% Indels: 0

DB: 5 Gaps: 0

US-10-079-954-2 (1-261) x ABG61944 (1-165)

QY 1 AGCCAGCAACGACGAGGTCACAAATAGAGTGTGGTGTCTCATGCTTGTGAGAGAGAAAC 60
 DB 31 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 50
 QY 61 ACTTTCGAGTGCAGAACCCAGAGGTCGAAATGAGCAGAGCCATCTGCGTTATAGCG 120
 DB 51 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTrpCysValIleAla 70
 QY 121 GCGGTGAAATATTTCACGTTTTTTCATGTTTCCACAGGTCTCCGCTGTTGTGCA 180
 DB 71 AlaValLysIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 90
 QY 181 GCGATGGAGAGACCCCAAGCAGAGAGAGCGGTTTTCTCTGGAAGGCCCATGCCCTTC 240
 DB 91 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 110
 QY 241 TTTTACCTCAAGTTGTATAA 261
 DB 111 PheTyrLeuLysCysCysLys 117
 RESULT 3
 ABUS6446
 ID ABUS6446 standard; protein; 165 AA.
 XX
 AC ABUS6446;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polypeptide #39.
 XX
 KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW intersitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 XX WO200286443-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 18-APR-2002; 2002WO-US012476.
 XX
 XX 18-APR-2001; 2001US-0284770P.
 XX
 XX 10-MAY-2001; 2001US-0280492P.
 XX
 XX 09-NOV-2001; 2001US-0339245P.
 XX
 XX 13-NOV-2001; 2001US-0350666P.
 XX
 XX 29-NOV-2001; 2001US-0334370P.
 XX
 XX 12-APR-2002; 2002US-0372246P.
 XX
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Aziz N, Murray R;
 XX
 XX WPI; 2003-093161/08.
 XX
 XX N-PSDB; ABX76167.
 XX
 XX Detecting a lung cancer-associated transcript in a cell from a patient
 XX for treating lung cancer, by contacting a biological sample from the
 XX patient with a polynucleotide that exhibits increased or decreased
 XX expression in lung cancer.
 XX
 XX Claim 27; Page 220; 453pp; English.
 XX
 XX The invention relates to a method for detecting a lung cancer-associated
 XX transcript in a cell from a patient, comprising contacting a biological
 XX sample from the patient with a polynucleotide that selectively hybridises
 XX to a sequence that is at least 80 % identical to a gene that exhibits
 XX increased or decreased expression in lung cancer samples. Lung cancer-
 XX associated polynucleotides and polypeptides are used for identifying a
 XX compound that modulates a lung cancer-associated polypeptide, for

CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX
 SQ Sequence 165 AA;
 Alignment Scores:
 Pred. No.: 1.7e-47 Length: 165
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: Gaps: 0
 US-10-079-954-2 (1-261) x ABUS6446 (1-165)
 QY 1 AGCCAGCAACGACGAGGTCACAAATAGAGTGTGGTGTCTCATGCTTGTGAGAGAGAAAC 60
 DB 31 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 50
 QY 61 ACTTTCGAGTGCAGAACCCAGAGGTCGAAATGAGCAGAGCCATCTGCGTTATAGCG 120
 DB 51 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTrpCysValIleAla 70
 QY 121 GCGGTGAAATATTTCACGTTTTTTCATGTTTCCACAGGTCTCCGCTGTTGTGCA 180
 DB 71 AlaValLysIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 90
 QY 181 GCGATGGAGAGACCCCAAGCAGAGAGAGCGGTTTTCTCTGGAAGGCCCATGCCCTTC 240
 DB 91 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 110
 QY 241 TTTTACCTCAAGTTGTATAA 261
 DB 111 PheTyrLeuLysCysCysLys 117
 RESULT 4
 ADN39436
 ID ADN39436 standard; protein; 165 AA.
 XX
 AC ADN39436;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A36.
 XX
 KW Human; differential expression; cancer; angiogenic disorder;
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
 KW inflammatory disease; autoimmune disease;
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;
 KW detection; diagnosis; prognosis; drug screening; drug targeting;
 KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;
 KW vulnery; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX WO2003042661-A2.
 XX
 XX 22-MAY-2003.
 XX
 XX 13-NOV-2002; 2002WO-US036810.
 XX
 XX 13-NOV-2001; 2001US-0350666P.
 XX
 XX 21-NOV-2001; 2001US-0332464P.
 XX

PR 29-NOV-2001; 2001US-0334393P.
 PR 03-DEC-2001; 2001US-0335394P.
 PR 14-DEC-2001; 2001US-0340376P.
 PR 08-JAN-2002; 2002US-0347211P.
 PR 10-JAN-2002; 2002US-0347349P.
 PR 08-FEB-2002; 2002US-0352509P.
 PR 13-FEB-2002; 2002US-0356714P.
 PR 20-FEB-2002; 2002US-0359077P.
 PR 29-MAR-2002; 2002US-0368809P.
 PR 04-APR-2002; 2002US-0370110P.
 PR 12-APR-2002; 2002US-0372248P.
 PR 05-JUN-2002; 2002US-0386614P.
 PR 16-JUL-2002; 2002US-0396839P.
 PR 22-JUL-2002; 2002US-0397755P.
 PR 22-JUL-2002; 2002US-0397845P.
 PR 09-SEP-2002; 2002US-0409450P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
 XX
 DR WPI; 2003-468649/44.
 DR N-PSDB; ADN39435.
 XX
 PT Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 PT a nucleic acid in a biological sample.
 XX
 PS Claim 12; SEQ ID NO A36; 1385pp; English.
 XX
 CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a polypeptide of the invention.
 XX
 SQ Sequence 165 AA;

Alignment Scores:
 Pred. No.: 1.7e-47 Length: 165
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 7 Gaps: 0

US-10-079-954-2 (1-261) x ADN39436 (1-165)

QY 1 AGCCAGCCGACGAGGGTGACATAGTGTGGTGTCTGCTGTGAGAGGAAAC 60
 DB 31 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 50
 QY 61 ACTTTCGAGTGCACAAACCCAGGAGGTGCAATGACAGAGCCATCTGGGTATAGCG 120
 DB 51 ThrPheGluCysGlnAsnProArgCysIysTrpThrGluProTrpCysValIleala 70
 QY 121 GCCGTGAAATATTTCCAGTTTTCATGGTTTCGCAACAGGTCTCCGCTGGTGTGCA 180
 DB 71 AlaValIysIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 90

QY 181 GCGATGAGAGAGCCCAAGCCAGAGGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTC 240
 DB 91 AlawetGluArgProIysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 110
 QY 241 TTTTACCTCAAGTGTGTAA 261
 DB 111 PheTyrlleuLysCysCysLys 117
 RESULT 5
 ADU06395
 ID ADU06395 standard; protein; 166 AA.
 XX
 AC ADU06395;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Novel bronchial cancer-associated human protein SeqID619.
 XX
 DE bronchial cancer; cytostatic; tumour-associated protein;
 KW cancer detection; metastasis; tumour; human.
 XX
 OS Homo sapiens.
 XX
 XX DE10316701-A1.
 XX
 XX 04-NOV-2004.
 XX
 XX 09-APR-2003; 2003DE-01016701.
 PF
 XX 09-APR-2003; 2003DE-01016701.
 XX
 XX (HINZ/) HINZMANN B.
 PA (HERM/) HERMANN K.
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.
 XX
 PI Mennerich D, Bruemendorf T, Heiden E, Hermann K, Kinnemann H;
 PI Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;
 XX
 XX WPI; 2004-786403/78.
 DR N-PSDB; ADU05908.
 XX

New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
 Claim 2; SEQ ID NO 619; 1381pp; German.

This invention relates to a novel isolated nucleic acid associated with bronchial cancer comprising 489 defined sequences given in the specification. The invention may be useful for the production of compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and the proteins/peptides encoded by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment (of tumours that have been stabilised or are no longer detectable).
 Detecting abnormal expression of the DNA sequences provides early diagnosis of bronchial cancers. The present sequence is that of a protein encoded by a novel bronchial cancer-associated human gene sequence of the invention.

SQ Sequence 166 AA;

Alignment Scores:
 Pred. No.: 1.71e-47 Length: 166
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 8 Gaps: 0

US-10-079-954-2 (1-261) x ADU06395 (1-166)

QY 1 AGCCAGCGAAGCGAGGTCACATAGAGTGTGTGTCATGTCGAGAGAGAAAC 60
 Db 31 SerGlnargThrAspGluGlyAspAsnargValTrpCysHisValCysGluargGluAsn 50
 QY 61 ACTTTCGAGTGCACAGAACCCAGAGGTCGAAATGGACAGAGCCATCTGCGTTATAGCG 120
 Db 51 ThrPheGluCysGlnAsnProargCysLysTrpThrGluProTrpCysValIleAla 70
 QY 121 GCCGTGAAATATTTCCAGGTTTTCATGTTCCCAACAGAGTGTCTCGCTGGTTGTGCA 180
 Db 71 AlaValLysIlePheProargPheMetValAlaLysGlnCysSerAlaGlyCysAla 90
 QY 181 GCGATGGAGAGACCCAGAGAGAGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTC 240
 Db 91 AlaMetGluargProLysProGluGluLysArgPheLeuLeuGluLuprometProphe 110
 QY 241 TTTTACCTCAAGTGTGTGAAA 261
 Db 111 PheTyrLeuLysCysCysLys 117

RESULT 6

AAW81754
 ID AAW81754 standard; protein; 223 AA.
 AC AAW81754;
 XX

DT 27-JAN-1999 (first entry)

XX Human Fanconi anaemia-associated gene II protein.

XX Fanconi anaemia gene II; immunogen; diagnosis; detection; disease;
 KW cell cycle; disorder; cell activation; DNA repair; cytopaenia;
 KW gene therapy; tumorigenesis.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 79
 FT Misc-difference /label= unknown
 FT Misc-difference 87
 FT Misc-difference /label= unknown

XX WO9845428-A1.

XX 15-OCT-1998.

XX 06-APR-1998; 98WO-EP001994.

XX 07-APR-1997; 97EP-00105688.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Kubbies M, Machl A, Planitzer S;

XX WPI; 1998-568348/48.

XX N-PSDB; AAV64572.

XX New human Fanconi anaemia associated gene-II - useful for diagnosis,
 FT treatment and prevention of diseases associated with abnormal cell
 FT cycling or activation, DNA repair, cytopaenia, tumorigenesis etc.

PS Claim 9; Page 20; 35pp; German.

XX This sequence represents a protein which is associated with Fanconi
 CC anaemia. This protein can be used as an immunogen for preparation of
 CC antibodies. This sequence can be used for diagnosis of, or detecting
 CC predisposition to, diseases that involve disorders of the cell cycle,
 CC cell activation, cell cycle progression, DNA repair, cytopaenia,
 CC tumorigenesis and/or tumour progression, also for treatment and
 CC prevention of these diseases, particularly by gene therapy

SQ Sequence 223 AA;

Alignment Scores:
 Pred. No.: 1.84e-47 Length: 223
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 2 Gaps: 0

US-10-079-954-2 (1-261) x AAW81754 (1-223)

QY 1 AGCCAGCGAAGCGAGGTCACATAGAGTGTGTGTCATGTCGAGAGAGAAAC 60
 Db 89 SerGlnargThrAspGluGlyAspAsnargValTrpCysHisValCysGluargGluAsn 108
 QY 61 ACTTTCGAGTGCACAGAACCCAGAGGTCGAAATGGACAGAGCCATCTGCGTTATAGCG 120
 Db 109 ThrPheGluCysGlnAsnProargCysLysTrpThrGluProTrpCysValIleAla 128
 QY 121 GCCGTGAAATATTTCCAGGTTTTCATGTTCCCAACAGAGTGTCTCGCTGGTTGTGCA 180
 Db 129 AlaValLysIlePheProargPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 QY 181 GCGATGGAGAGACCCAGAGAGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTC 240
 Db 149 AlaMetGluargProLysProGluGluLysArgPheLeuLeuGluLuprometProphe 168
 QY 241 TTTTACCTCAAGTGTGTGAAA 261
 Db 169 PheTyrLeuLysCysCysLys 175

RESULT 7

ABR48226
 ID ABR48226 standard; protein; 223 AA.
 XX AC ABR48226;
 XX

DT 12-JUN-2003 (first entry)

XX Human bladder cancer associated protein sequence SEQ ID NO:173.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO2003003906-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021338.

XX 03-JUL-2001; 2001US-0302814P.

XX 03-AUG-2001; 2001US-0310099P.

XX 08-NOV-2001; 2001US-0343705P.

XX 13-NOV-2001; 2001US-0350666P.

XX 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Aziz N;

XX WPI; 2003-201532/19.

XX N-PSDB; ACC51042.

XX

XX Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.

PS Claim 10; Page 289; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises

CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytosolic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications
 XX
 SQ Sequence 223 AA;

Alignment Scores:
 Pred. No.: 1.84e-47 Length: 223
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: Gaps: 0

US-10-079-954-2 (1-261) x ABR48226 (1-223)

QY 1 AGCCAGCGACGACGAGGGTGACATAGAGTGTGTCTCATGTGTGAGAGAGAAAC 60
 DB 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
 QY 61 ACTTTCGAGTCCGACGACCCAGGAGGTCGAAATGACAGAGCCATCTGCGTGTATAGCG 120
 DB 109 ThrPheGluCysGlnAsnProArgArgCysIstPrThrGluProTrpCysValIleAla 128
 QY 121 GCGTGAAATATTTCCACGTTTTCATGTTTCGACAGAGTGTCTCGCTGGTGTGCA 180
 DB 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 QY 181 GCGATGGAGAGACCCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 149 AlaMetGluArgProLysProGluLysArgPheLeuLeuGluGluProMetProphe 168
 QY 241 TTTTACCTCAAGTGTGTAAA 261
 DB 169 PheTyrLeuLysCysCysLys 175

RESULT 8
 ABUS56671
 ID ABUS56671 standard; protein; 223 AA.
 XX
 AC ABUS56671;
 XX
 XX
 DT 02-APR-2003 (first entry)
 XX
 XX
 DE Lung cancer-associated polypeptide #264.
 XX
 KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; asthma; fibrosis; bronchiectasis.
 XX
 OS Unidentified.
 XX
 XX WO200286443-A2.
 XX
 XX 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX
 XX 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 , PR

PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0324370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Aziz N, Murray R;
 XX
 XX WPI; 2003-093161/08.
 DR N-PSDB; ABX76400.
 XX
 XX Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX

Claim 27; Page 392; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABUS56408-ABUS56745 represent lung cancer-associated polypeptides of the invention

SQ Sequence 223 AA;

Alignment Scores:
 Pred. No.: 1.84e-47 Length: 223
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: Gaps: 0

US-10-079-954-2 (1-261) x ABUS56671 (1-223)

QY 1 AGCCAGCGACGACGAGGGTGACATAGAGTGTGTCTCATGTGTGAGAGAGAAAC 60
 DB 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
 QY 61 ACTTTCGAGTCCGACGACCCAGGAGGTCGAAATGACAGAGCCATCTGCGTGTATAGCG 120
 DB 109 ThrPheGluCysGlnAsnProArgArgCysIstPrThrGluProTrpCysValIleAla 128
 QY 121 GCGTGAAATATTTCCACGTTTTCATGTTTCGACAGAGTGTCTCGCTGGTGTGCA 180
 DB 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 QY 181 GCGATGGAGAGACCCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 149 AlaMetGluArgProLysProGluLysArgPheLeuLeuGluGluProMetProphe 168
 QY 241 TTTTACCTCAAGTGTGTAAA 261
 DB 169 PheTyrLeuLysCysCysLys 175

RESULT 9
 ADN39022
 ID ADN39022 standard; protein; 223 AA.

CC a host cell genetically engineered to comprise (I) which is operatively
CC associated with a regulatory sequence that modulates expression of (I) in
CC the host cell; (4) a polypeptide (II) encoded by (1); (5) a composition
CC comprising the polypeptide of (4) and a carrier; (6) an antibody directed
CC against the polypeptide of (4); (7) detecting (1) or the polypeptide of
CC (4) in a sample; (8) identifying a compound that binds to the polypeptide
CC of (4); (9) producing the polypeptide of (4); and (10) a collection of
CC polynucleotides comprising at least one of the polynucleotide sequences
CC (I). The polynucleotides (I) can be used as hybridisation probes,
CC oligomers or primers, for chromosome or gene mapping, for the recombinant
CC production of proteins, and for generating antisense DNA or RNA. The
CC present sequence represents a human contig polypeptide sequence, which is
CC used in an example from the present invention.

XX SQ Sequence 248 AA;

Alignment Scores: 1.89e-47 Length: 248
Pred. No.: 482.00 Matches: 83
Score: 96.6% Conservative: 1
Percent Similarity: 95.4% Mismatches: 3
Best Local Similarity: 96.0% Indels: 0
Query Match: 7 Gaps: 0
DB:

US-10-079-954-2 (1-261) x ADF60487 (1-248)

QY 1 AGCCAGCGAAGCGAGCGGTGACATAGAGTGTGGTGTCTGAGAGAGAAAC 60
DB 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
QY 61 ACTTTCGAGTCCGAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGAGAGAGAAAC 120
DB 109 ThrPheGluCysGlnAsnProArgArgCysLysTrpThrGluProTyrCysValIleAla 128
QY 121 GCCGTGAAATATTTCCACGTTTTTTCATGCTGCGCAACAGCGTCTCGCTGGTGTGCA 180
DB 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
QY 181 GCGATGGAGAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGAGAGAGAAAC 240
DB 149 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 168
QY 241 TTTTACCTCAAGTGTGTAAA 261
DB 169 PheTyrLeuLysCysCysLys 175

RESULT 11

ID ADF59395

XX ADF59395 standard; protein; 171 AA.

AC ADF59395;

XX 12-FEB-2004 (first entry)

DE Human therapeutic contig protein - SEQ ID 2489.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..248

FT /label= Unknown, OTHER

FT /note= "OTHER = In-frame stop codon"

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX

PR 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren P, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
PI WPI; 2004-658857/65.
XX N-PSDB; ADS11654.

XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.

XX Example 2; SEQ ID NO 2489; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnery activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic contig
XX protein of the invention.

XX SQ Sequence 248 AA;

Alignment Scores: 1.89e-47 Length: 248
Pred. No.: 482.00 Matches: 83
Score: 96.6% Conservative: 1
Percent Similarity: 95.4% Mismatches: 3
Best Local Similarity: 96.0% Indels: 0
Query Match: 8 Gaps: 0
DB:

US-10-079-954-2 (1-261) x ADS12252 (1-248)

QY 1 AGCCAGCGAAGCGAGCGGTGACATAGAGTGTGGTGTCTGAGAGAGAAAC 60
DB 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
QY 61 ACTTTCGAGTCCGAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGAGAGAGAAAC 120
DB 109 ThrPheGluCysGlnAsnProArgArgCysLysTrpThrGluProTyrCysValIleAla 128
QY 121 GCCGTGAAATATTTCCACGTTTTTTCATGCTGCGCAACAGCGTCTCGCTGGTGTGCA 180
DB 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
QY 181 GCGATGGAGAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGAGAGAGAAAC 240
DB 149 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 168
QY 241 TTTTACCTCAAGTGTGTAAA 261
DB 169 PheTyrLeuLysCysCysLys 175

RESULT 12

ADFS9395

ID ADFS9395 standard; protein; 171 AA.

XX ADFS9395;

XX 12-FEB-2004 (first entry)

XX Human polypeptide sequence SEQ ID NO:1803.

XX biological activity; genetic engineering; hybridisation probe; oligomer;
XX primer; chromosome mapping; gene mapping; recombinant protein production;
XX human.

XX Homo sapiens.


```
QY 241 TTTTACCTCAAGTGTG 257
Db |||||
157 euLeuProGlnValIeu 162

RESULT 14
AD117070
ID AD117070 standard, protein, 154 AA.
XX AC AD117070;
XX DT 15-APR-2004 (first entry)
XX DE Murine NOVX protein homologue SeqID 606.
XX KW mouse; murine; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; achma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infect.
XX OS Mus musculus.
XX PN WO200268649-A2.
XX PD 06-SEP-2002.
XX PF 31-JAN-2002; 2002WO-US002785.
XX PR 31-JAN-2001; 2001US-026539SP.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 02-FEB-2001; 2001US-0265517P.
PR 05-FEB-2001; 2001US-0266406P.
PR 07-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-027875P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0280992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.

21-AUG-2001; 2001US-0313390P.
28-AUG-2001; 2001US-0315470P.
31-AUG-2001; 2001US-0316447P.
07-SEP-2001; 2001US-0318115P.
12-SEP-2001; 2001US-0318118P.
12-SEP-2001; 2001US-0318740P.
19-SEP-2001; 2001US-0323379P.
18-OCT-2001; 2001US-0330245P.
18-OCT-2001; 2001US-0330308P.
14-NOV-2001; 2001US-0332701P.
(CURA-) CURAGEN CORP.
Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
Gielach V, Taupier R, Gusev V, Colman SD, Wolenc AR, Pena CE;
Furtak K, Grosse WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
WPI; 2002-706998/76.
New NOVX polypeptides and nucleic acids, useful for preventing or
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
pharmacogenomics.
Disclosure; SEQ ID NO 606; 1498pp; English.
This invention relates to a novel nucleic acids, and encoded polypeptides
thereof, which have properties related to the stimulation of biochemical
or physiological responses in a cell, tissue, organ or organism.
Specifically, it refers to the use of biologically active fragments for
diagnostic and prognostic assays and furthermore in the treatment of
diverse pathological conditions. The present invention describes novel
human and murine NOVX proteins, as well as methods to modulate their
expression using antisense oligos, ribozymes and peptide nucleic acids.
The NOVX polypeptides, polynucleotides and antibodies are useful in
treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
atherosclerosis, cancer and diabetes. Furthermore, they may be used in
treating or preventing diseases such as inflammation, autoimmune
disorders, allergies, blood disorders, acquired immunodeficiency syndrome
(AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
and epilepsy. Accordingly, these molecules have many activities including
cytostatic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
antiasthmatic, nephrotropic, antiarthritic, virucide, antiparasitic,
neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
relaxant and anticonvulsant. In addition, they are useful in screening
assays to identify small molecules that modulate or inhibit, for example,
neurogenesis, wound healing and angiogenesis. The nucleic acids are also
used as in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
of the invention.
SQ Sequence 154 AA;

Alignment Scores:
Pred. No.: 5.77e-15 Length: 154
Score: 205.00 Matches: 33
Percent Similarity: 57.6% Conservative: 16
Best Local Similarity: 38.8% Mismatches: 30
Query Match: 40.8% Indels: 6
DB: Gaps: 1

US-10-079-954-2 (1-261) x AD117070 (1-154)
QY 25 AATAGAGTGTGTCATGCTTGTGAGAGAGAAACACTTTCGAGTGCCAGAACCAAGG 84
Db |||||
19 AsnAlaIeuThrCysHisValCysGluAlaGlnAsnSerTyrAlaCysSerAsnProSer 38
QY 85 AGGTGCAATGAGACAGACCCATCTGCGTTATAGCGCGCCGTGAATAATTTCCACGTTT 144
Db |||||
39 GlnCysProGlyGluLysPheCysLeuLeuAlaValThrArgIlePheGluArgPhe 58
```


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Result No.	Query			Description	
	Score	Match Length	ID	DB	ID
1	482	96.0	162	4	US-10-264-049-3898
2	482	96.0	165	4	Sequence 3898, Ap
3	482	96.0	223	3	Sequence 754, App
4	482	96.0	223	3	Sequence 2, Appli
5	482	96.0	223	4	Sequence 2, Appli
6	482	96.0	223	4	Sequence 340, App
7	482	96.0	223	4	Sequence 173, App
8	205	40.8	154	4	Sequence 4, Appli
9	81	16.1	240	4	Sequence 606, App
10	80	15.9	583	4	Sequence 3710, Ap
11	77.5	15.4	106	4	Sequence 6181, A


```
Db 149 AlametGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProphe 168
Qy 241 TTTTACCTCAAGTGTGTAAA 261
Db 169 PheTyrLeuLysCysCysLys 175

RESULT 4
US-10-199-448-2
; Sequence 2, Application US/10199448
; Publication No. US20030022858A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Mannheim GmbH
; TITLE OF INVENTION: Fanconi-gene II
; NUMBER OF SEQUENCES: 2
; STREET: Sandhofer Str. 112-132
; CITY: Mannheim
; COUNTRY: Germany
; ZIP: 68305
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,448
; FILING DATE: 19-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,801
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/09/402,632
; FILING DATE: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-199-448-2

Alignment Scores:
Pred. No.: 2,36e-50 Length: 223
Score: 482.00 Matches: 83
Percent Similarity: 96.4% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 4 Gaps: 0

US-10-079-954-2 (1-261) x US-10-199-448-2 (1-223)
Qy 1 AGCCAGCGAACGCGAGGGTGACATAGAGTGTGTCATGCTTGTGAGAGAAAC 60
Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
Qy 61 ACTTTCCAGTCCAGAACCCCAAGAGGTGCAATAGGACAGCCATACCTCGTTATAGCG 120
Db 109 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTyrCysValIleAla 128
Qy 121 GCCGTGAAATATTTCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGTGTGCA 180
Db 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
Qy 181 GCGATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCCATGCCCTTC 240
Db 149 AlametGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProphe 168
Qy 241 TTTTACCTCAAGTGTGTAAA 261
Db 169 PheTyrLeuLysCysCysLys 175

RESULT 5
US-10-295-027-340
```

```
; Sequence 340, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 340
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-340

Alignment Scores:
Pred. No.: 2,36e-50 Length: 223
Score: 482.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 4 Gaps: 0

US-10-079-954-2 (1-261) x US-10-295-027-340 (1-223)
Qy 1 AGCCAGCGAACGCGAGGGTGACATAGAGTGTGTCATGCTTGTGAGAGAAAC 60
Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
Qy 61 ACTTTCCAGTCCAGAACCCCAAGAGGTGCAATAGGACAGCCATACCTCGTTATAGCG 120
Db 109 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTyrCysValIleAla 128
Qy 121 GCCGTGAAATATTTCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGTGTGCA 180
Db 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
Qy 181 GCGATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCCATGCCCTTC 240
Db 149 AlametGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProphe 168
```



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; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 606
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-072-012-606

Alignment Scores:
Pred. No.: 4,24e-16 Length: 154
Score: 205.00 Matches: 33
Percent Similarity: 57.6% Conservative: 16
Best Local Similarity: 38.8% Mismatches: 30
Query Match: 40.8% Indels: 6
DB: 4 Gaps: 1

US-10-079-954-2 (1-261) x US-10-072-012-606 (1-154)
Qy 25 AATGAGTGGTGTCTGATGAGAGAGAAACACTTTCGAGTGCCAGAACCCAGG 84
Db 19 AsnAlaLeuThrCysHisValCysGluAlaGlnAsnSerTyAlaCysSerAsnProSer 38
Qy 85 AGGTGCAATGCAGACAGCCACTCTGCTTATAGCGCGCGTGAATAATTTCCACGTTT 144
Db 39 GlnCysProGlyGluLysLysPheCysLeuLeuAlaValThrArgIlePheGluArgPhe 58
Qy 145 TTCATGGTTCGAACAGGTGCTCCGCTGGTTGTGCAGCG-----ATG 186
Db 59 PheTyValSerLysGlnCysThrArgCysProThrProValValSerProProSer 78
Qy 187 GAGAGACCCAGCCAGGAGAGAGCGTTTCTCTGGAAGCCCATGCCCTTTTAC 246
Db 79 ThrAsnProProSerGluProLysGluPheLeuIleGluLysProMetProPheLeuPhe 98
Qy 247 CTCAGTGTCTTAA 261
Db 99 TyrLysCysGln 103

RESULT 9
US-10-369-493-3710
; Sequence 3710, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3710
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(240)
; OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-3710

Alignment Scores:
Pred. No.: 1.06 Length: 240
Score: 81.00 Matches: 18
Percent Similarity: 47.2% Conservative: 7
Best Local Similarity: 34.0% Mismatches: 20
Query Match: 16.1% Indels: 8
DB: 4 Gaps: 2

US-10-079-954-2 (1-261) x US-10-369-493-3710 (1-240)
Qy 1 AGCCAGCGAACGACGAGGCGTGACATAGAGTGGTGTCTGCTGTGAGAGAGAAAC 60
Db 179 SerGlnHisThrAspProThrAsnGlnArgIleTrpValTyrSerThrGln----- 195
Qy 61 ACTTTCGAGTGCCAGAACCCAGGAGGTGCATAATGGACAGAGCCCATCTGCTTATAGCG 120
Db 196 -----GluAsnPro----SerAlaProTrpLysGluMetTyrCysPheAlaAla 210
Qy 121 GCCGTGAAATATATTCACGCTTTTTCATGCTGTCGCAAC 159
Db 211 AspThrGluPhePheProAlaAspPheGluValMetAsn 223

RESULT 10
US-10-282-122A-61811
; Sequence 61811, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 61811
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-61811

Alignment Scores:
Pred. No.: 1.76 Length: 583
Score: 80.00 Matches: 21
Percent Similarity: 43.7% Conservative: 10
Best Local Similarity: 29.6% Mismatches: 30
Query Match: 15.9% Indels: 10
DB: 4 Gaps: 1

US-10-079-954-2 (1-261) x US-10-282-122A-61811 (1-583)
QY 66 CGAGTGCAGCAACCCAGGAG-----GTGCAATG 95
Db 294 ArgValHisGluProHisGluThrValArgIleAlaLeuValGlyLysTyrValGluLeu 313
QY 96 GACAGGCATCTCGTGGTTATAGCGCGGTGAAATATTTCCACGTTTTTTCATGGTTCG 155
Db 314 SerAspAlaTyrLeuSerValThrGluAlaLeuArgAlaGlyPhePheHisAla 333
QY 156 CAACAGGTGTCGCGTGGTTGTGCAGCGATGAGACCCAGCCAGGAGAGCGGTT 215
Db 334 LysValGluMetValTyrValAlaSerAspAspCysGluSerAlaSerGlyAlaAla 353
QY 216 TCTCTGGAAGACCCATGCGCTTTTACT 248
Db 354 AlaLeuGlyGluValHisGlyValLeuIlePro 364

RESULT 11
US-10-437-963-174792
; Sequence 174792, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174792
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_726C.1.pep
US-10-437-963-174792

Alignment Scores:
Pred. No.: 2.36 Length: 106
Score: 77.50 Matches: 23
Percent Similarity: 39.2% Conservative: 6
Best Local Similarity: 31.1% Mismatches: 30
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```
Query Match: 15.4% Indels: 15
DB: 4 Gaps: 4

US-10-079-954-2 (1-261) x US-10-437-963-174792 (1-106)
QY 40 CATGCTGTGAGAGAGAAAACATTTCGAGTGCAGAACCCA----- 81
Db 24 HisArgCysHisArgHisArgGlyTyrArgLeuGluGlnProGlyGlnAsnHisAlaLeu 43
QY 82 -----AGGAGGTGCAATGGACAGACGCCATCTGCTTATAGCGCGTGA--- 129
Db 44 CysSerGlyGlyArgCysGlnTyrArgTyrArgHisCysValGlnAlaAlaThrSerPro 63
QY 130 ATATTTCACGTTTTTTCATGGTTCCCAACAGGTGCTCCCGTGTGTGCGAGCGATGAG 189
Db 64 LeuLeuProArgAlaPheSer---ArgSerArgMetLeuGlyAlaAlaThrAlaProPro 82
QY 190 AGACCCCAAGCCAGAGGAGAGCGGTTTCTCTCGAAGAGGCC 231
Db 83 ArgProProProAlaArg-----TyrGluGluPro 92

RESULT 12
US-10-282-122A-45313
; Sequence 45313, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 45313
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: {151}..(151)
; OTHER INFORMATION: X=any amino acid
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FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (280)..(280)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (302)..(302)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (561)..(561)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (620)..(620)
OTHER INFORMATION: X=any amino acid
US-10-282-122A-45313
Alignment Scores:
Pred. No.: 7.47 Length: 636
Score: 75.00 Matches: 27
Percent Similarity: 48.8% Conservative: 14
Best Local Similarity: 32.1% Mismatches: 32
Query Match: 14.9% Indels: 11
DB: 4 Gaps: 2
US-10-079-954-2 (1-261) x US-10-282-122A-45313 (1-636)
Qy 254 CACTTGAGTAAAGAGGCGATGGCTCTCCAGGAGAACCCCTCTCTCTGGCTTG 195
Db 93 HisalagGlyGlyspheGlyGlnGlyGlyTyrLysThrSerGlyGlyLeuHisGlyVal 112
Qy 194 GGTCTCTCCATCGCTGCACACACGAGCGAGCACCTGTTGCGAACCATGAAACGTTGA 135
Db 113 GlyalaserValvalaenAlaLeuSerGluTrpLeuValThrIleLysArgAspGly 132
Qy 134 AATATTTTCAGCGCGCTATACACGATGCTCTGTCATTGTCACCTCTCTGGGT-- 77
Db 133 AsnIleTyrGluHisAlaLeuLeuGlyGly-ValProValThrThrSerLeu**Ly 152
Qy 76 -----TCTGCACCTCGAAGTGTCTTCTCTCTCACAGCATGACAC 36
Db 152 sIleGlyLysThrLysGluSerGlyThrThrMetHisPhe-----LysProAspTh 169
Qy 35 CACACTCTAT 26
Db 169 rThrIlePhe 172
RESULT 13
US-10-437-963-124768
Sequence 124768, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 124768
LENGTH: 326
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_27475C.1.pep
US-10-437-963-124768
Alignment Scores:
Pred. No.: 11.2 Length: 326
Score: 73.00 Matches: 12
Percent Similarity: 71.4% Conservative: 8
Best Local Similarity: 42.9% Mismatches: 8
Query Match: 14.5% Indels: 0
DB: 4 Gaps: 0
US-10-079-954-2 (1-261) x US-10-437-963-124768 (1-326)
Qy 167 GAGCACCTGTTGCGAACCATGAAACCGTGGAAATATTTTCACGGCCGTATAACCGAG 108
Db 188 GlnSerLeuValAspArgLeuLysAsnValGlyAspLeuLeuThrValAlaValThrGln 207
Qy 107 TATGGCTCTGTCATTGTCACCTC 84
Db 208 TyrGlyAspLeuHisLeuHisVal 215
RESULT 14
US-09-746-783-218
Sequence 218, Application US/09746783
Publication No. US20030044935A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Fechtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-746-783-218
Alignment Scores:
Pred. No.: 13.1 Length: 342
Score: 72.50 Matches: 24
Percent Similarity: 45.0% Conservative: 12
```

```
Best Local Similarity: 30.0%      Mismatches: 29
Query Match: 14.4%             Indels: 15
DB: 3                          Gaps: 4

US-10-079-954-2 (1-261) x US-09-746-783-218 (1-342)

QY 22 GACAAATAGAGTGGTGTGTCATGCTTGCAGAGAGAAACACTTTCGAGTGCAGAACCCA 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 AspArgAlaValLeuIleSerAlaCysGluArg-----GlyCysArgLeuPhe 84
QY 82 AGGAGGTGCAATGG-----ACAGAGCCCATCTGCGTT 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 SerIleCysArgPheValAlaArgSerSerLysProAsnAlaThrGlnThrGluCysGlu 104
QY 115 ATAGCGCGCGTGAATAATATTTCCAGTGTTCATGTTTCGCAACAGAGTGCCTCGCTGGT 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 AlaAlaCysValGluAlaTyxValLys---GluAlaGluGlnGlnAlaCysSerHisGly 123
QY 175 TGT---GCAGCGATGGAGAGACCCAGCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCC 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 CysTrpSerGlnProAlaGluProGluProGluGlnLysArgLysValLeuGluAlaPro 143

RESULT 15
US-10-296-115-1297
; Sequence 1297, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1297
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1297

Alignment Scores:
Pred. No.: 13.2      Length: 353
Score: 72.50      Matches: 24
Percent Similarity: 45.0%      Conservative: 12
Best Local Similarity: 30.0%      Mismatches: 29
Query Match: 14.4%      Indels: 15
DB: 4              Gaps: 4

US-10-079-954-2 (1-261) x US-10-296-115-1297 (1-353)

QY 22 GACAAATAGAGTGGTGTGTCATGCTTGCAGAGAGAAACACTTTCGAGTGCAGAACCCA 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 AspArgAlaValLeuIleSerAlaCysGluArg-----GlyCysArgLeuPhe 95
QY 82 AGGAGGTGCAATGG-----ACAGAGCCCATCTGCGTT 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 SerIleCysArgPheValAlaArgSerSerLysProAsnAlaThrGlnThrGluCysGlu 115
QY 115 ATAGCGCGCGTGAATAATATTTCCAGTGTTCATGTTTCGCAACAGAGTGCCTCGCTGGT 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 AlaAlaCysValGluAlaTyxValLys---GluAlaGluGlnGlnAlaCysSerHisGly 134
QY 175 TGT---GCAGCGATGGAGAGACCCAGCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCC 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 CysTrpSerGlnProAlaGluProGluProGluGlnLysArgLysValLeuGluAlaPro 154
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Search completed: March 23, 2006, 12:54:45
Job time : 80.5807 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:49:19 ; Search time 2.15161 Seconds
(without alignments)
694.416 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 502

Sequence: 1 agccaggaacggagcagg.....tttacctcaagtgtgtaaa 261

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 339260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/abss/ABSSWEB-epool/US10079954/runat_23032006_102937_1988/app_query.fasta_1
-DB=Published Applications AA New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10079954@CGN_1_24 @runat_23032006_102937_1988 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSFBLOCKS=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA New.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.5	14.4	342	6	US-10-689-742-218
2	68	13.5	1476	6	US-10-647-956A-4
3	66.5	13.2	178	6	US-10-892-379-4
C 4	66	13.1	366	6	US-10-055-877-302
C 5	66	13.1	469	6	US-10-063-703-58
C 6	66	13.1	469	7	US-11-102-240-58
C 7	66	13.1	469	7	US-11-103-195-58
8	66	13.1	906	7	US-11-124-635-4
9	66	13.1	934	7	US-11-077-386-17

10	66	13.1	1390	6	US-10-957-351-1	Sequence 1, Appli
11	66	13.1	1408	7	US-11-072-175-186	Sequence 186, App
12	65.5	13.0	618	7	US-11-078-735-18	Sequence 18, Appl
13	65.5	13.0	618	7	US-11-050-346-63	Sequence 63, Appl
14	65.5	13.0	618	7	US-11-103-077-18	Sequence 18, Appl
C 15	65	12.9	430	7	US-11-087-099-12253	Sequence 12253, A
16	65	12.9	858	6	US-10-878-556A-113	Sequence 113, App
17	64.5	12.8	73	5	US-09-978-360A-578	Sequence 578, App
18	64	12.7	169	7	US-11-096-568A-12447	Sequence 12447, A
19	64	12.7	174	7	US-11-096-568A-12446	Sequence 12446, A
C 20	64	12.7	350	7	US-11-087-099-2497	Sequence 2497, Ap
C 21	64	12.7	350	7	US-11-087-099-11952	Sequence 11952, A
22	63.5	12.6	533	6	US-10-467-657-8	Sequence 8, Appli
23	63.5	12.6	567	6	US-10-467-657-4328	Sequence 4328, Ap
24	63.5	12.6	1379	7	US-11-114-962-4	Sequence 4, Appli
25	63	12.5	166	7	US-11-176-830-255	Sequence 255, App
C 26	63	12.5	517	7	US-11-037-243-76	Sequence 76, Appl
C 27	63	12.5	1074	7	US-11-087-099-1585	Sequence 1585, Ap
28	62.5	12.5	757	6	US-10-055-877-190	Sequence 190, App
29	62	12.4	166	7	US-11-176-830-1198	Sequence 1198, Ap
30	62	12.4	166	7	US-11-196-067-394	Sequence 394, App
C 31	62	12.4	756	6	US-10-055-877-34	Sequence 34, Appl
C 32	62	12.4	756	6	US-10-055-877-187	Sequence 187, App
C 33	62	12.4	756	6	US-10-055-877-188	Sequence 188, App
C 34	62	12.4	756	6	US-10-055-877-189	Sequence 189, App
C 35	62	12.4	830	6	US-10-055-877-32	Sequence 32, Appl
C 36	61.5	12.3	196	6	US-10-967-527A-27	Sequence 27, Appl
37	61.5	12.3	323	7	US-11-240-769-103	Sequence 103, App
C 38	61	12.2	60	5	US-09-978-360A-592	Sequence 592, App
C 39	61	12.2	181	7	US-11-096-568A-27033	Sequence 27033, A
C 40	60.5	12.1	337	7	US-11-096-568A-7804	Sequence 7804, Ap
C 41	60.5	12.1	342	7	US-11-096-568A-7803	Sequence 7803, Ap
C 42	60.5	12.1	501	7	US-11-096-568A-7802	Sequence 7802, Ap
C 43	60.5	12.1	960	7	US-11-169-041-177	Sequence 177, App
44	60	12.0	66	7	US-11-172-536-1	Sequence 1, Appli
45	60	12.0	97	7	US-11-172-536-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-689-742-218
; Sequence 218, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 218
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-218
Alignment Scores:
Pred. No.: 1.44 Length: 342
Score: 72.50 Matches: 24
Percent Similarity: 45.0% Conservative: 12
Best Local Similarity: 30.0% Mismatches: 29
Query Match: 14.4% Indels: 15

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DB:
US-10-079-954-2 (1-261) x US-10-689-742-218 (1-342)
QY 22 GACATAGAGTGTGGTGTGTCATGTCGTGTCAGAGAGAAACACTTTTCGAGTGCAGAACCCA 81
Db 69 AspArgAlaValLeuIleSerAlaCysGluArg-----GlyCysArgLeuPhe 84
QY 82 AGGAGGTCCAATGG-----ACAGAGCCCATCTGCGTT 114
Db 85 SerIleCysArgPheValAlaArgSerSerIysProAenAlaThrGlnThrGluCysGlu 104
QY 115 ATAGGGCCGTGAAATATTTCCAGTTCATGTTTCATGGTTCACACAGGTGCTCCGCTGGT 174
Db 105 AlaAlaCysValGluAlaTyrValLys---GluAlaGluGlnGlnAlaCysSerHisGly 123
QY 175 TGT---GCAGCGATGGAGAGACCCCAAGCCAGAGAGAGCGGTTTCTCTCGAAGAGGCC 231
Db 124 CysTTPSerGlnProAlaGluProGluProGluGlnLysArgLysValLeuGluAlaPro 143
RESULT 2
US-10-647-956A-4
; Sequence 4, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647,956A
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 1476
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-10-647-956A-4
Alignment Scores:
Pred. No.: 5.37 Length: 1476
Score: 68.00 Matches: 23
Percent Similarity: 42.9% Conservative: 7
Best Local Similarity: 32.9% Mismatches: 22
Query Match: 13.5% Indels: 18
DB: 6 Gaps: 3
US-10-079-954-2 (1-261) x US-10-647-956A-4 (1-1476)
QY 53 GAGAAAACACTTTCAGTGCAGAACCCAGAGGTGCAATGACAGAGCCATCTACTCG 112
Db 791 GluGlnThrAspSerHisGlnLeuAlaGlnGlyAsnAlaProGluArgThrProAla 810
QY 113 TTATAGCGCGCGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTG 172
Db 811 LeuThrLys-----SerTTPyrAlaThrGlyLeuProAla 822
QY 173 GTT-----GTGAGCGATGGAGAGACCCCAAGCCAGAGAGAGCGGTTTC 217
Db 823 ValAspAsnAlaLeuSerAlaGlyTyrTTPArgGlyAspLysGlnAlaPheAlaGlyPhe 842
QY 218 TCCTGGAGAGCCCATGCTCTTTTACC 247
Db 843 Thr-----ProArgPheThr 847
RESULT 3
US-10-892-379-4
; Sequence 4, Application US/10892379
; Publication No. US20050282999A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Ozenberger, Bradley A.
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Kajkowski, Eileen M.
; APPLICANT: Jacobsen, Jack S.
; APPLICANT: Walker, Stephen G.
; APPLICANT: Sophia, Heidi
; APPLICANT: Howland, David
; TITLE OF INVENTION: Beta-Amyloid Peptide-Binding Proteins and Polynucleotides
; FILE REFERENCE: 31896-67300 (AHP98128P2 Cl)
; CURRENT APPLICATION NUMBER: US/10/892,379
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 09/852,100
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/774,936
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: US 09/172,990
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: US 09/060,609
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: US 60/064,583
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-892-379-4
Alignment Scores:
Pred. No.: 6.9 Length: 178
Score: 66.50 Matches: 16
Percent Similarity: 42.1% Conservative: 0
Best Local Similarity: 42.1% Mismatches: 17
Query Match: 13.2% Indels: 5
DB: 6 Gaps: 1
US-10-079-954-2 (1-261) x US-10-892-379-4 (1-178)
QY 10 ACGAGCAGCGTGACATAGAGTGTGTCATGTCGTGTCAGAGAGAAACACTTTTCGAG 69
Db 53 ThrArgGluGlyArgAlaArgValTTPCysIleAlaAlaAsnGluIleAsnCysThrGlu 72
QY 70 TGCAGAACCCCAAGG-----AGGTGCAAAATCGACAGAGCCCATAC 108
Db 73 ThrGlyAsnAlaThrPheThrArgGluValProCysLysTTPThrAsnGlyTyr 90
RESULT 4
US-10-055-877-302
; Sequence 302, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Wei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
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; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinketo, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 302
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-055-877-302

Alignment Scores:
Pred. No.:      8.32      Length:      366
Score:          66.00     Matches:      17
Percent Similarity: 51.7%  Conservative: 14
Best Local Similarity: 28.3% Mismatches:    19
Query Match:    13.1%     Indels:       10
DB:              3       Gaps:         3

US-10-079-954-2 (1-261) x US-10-055-877-302 (1-366)
Qy 197 TTGGTCTCTCCATCGTCACACGAGCAGCCTGTTCGAAACCATGAAAAACGT 138
Db 7 LeuGlyVallyslleSerGluGlnGlnAluLysleuLysSerMetAspLysAsn 26
Qy 137 GGAATATTTTCACGCGCGCTATACGCGATGATGCTCTGTCCATTTG----- 90
Db 27 GlyThrMet---ThrIleAspTrpAsnGluTrpArgAspTyrHisLeuLeuHisProVal 45
Qy 89 -----CACCTCTGGTCTCGG---CACTCGAAAGTGTTCCTCTCTCAAA 45
Db 46 GluAsnIleProGluIleLeuTyrTrpLysHisSerThrIlePheAspValGlyGlu 65

RESULT 5
US-10-063-703-58
; Sequence 58, Application US/10063703
; Publication No. US20060008901A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-58

Alignment Scores:
Pred. No.:      8.47      Length:      469
Score:          66.00     Matches:      17
Percent Similarity: 51.7%  Conservative: 14
Best Local Similarity: 28.3% Mismatches:    19
Query Match:    13.1%     Indels:       10
DB:              3       Gaps:         3

US-10-079-954-2 (1-261) x US-10-063-703-58 (1-469)
Qy 197 TTGGTCTCTCCATCGTCACACGAGCAGCCTGTTCGAAACCATGAAAAACGT 138
Db 110 LeuGlyVallyslleSerGluGlnGlnAluLysleuLysSerMetAspLysAsn 129
Qy 137 GGAATATTTTCACGCGCGCTATACGCGATGATGCTCTGTCCATTTG----- 90
Db 130 GlyThrMet---ThrIleAspTrpAsnGluTrpArgAspTyrHisLeuLeuHisProVal 148
Qy 89 -----CACCTCTGGTCTCGG---CACTCGAAAGTGTTCCTCTCTCAAA 45
Db 149 GluAsnIleProGluIleLeuTyrTrpLysHisSerThrIlePheAspValGlyGlu 168

RESULT 6
US-11-102-240-58
; Sequence 58, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-58
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; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-077-386-17

Alignment Scores:
Pred. No.:      8.91      Length:      934
Score:          66.00     Matches:      18
Percent Similarity: 38.2% Conservative: 8
Best Local Similarity: 26.5% Mismatches: 31
Query Match:     13.1% Indels:      11
DB:              7       Gaps:       2

US-10-079-954-2 (1-261) x US-11-077-386-17 (1-934)

Qy 34 TGGTGTCTATGCTTGTGAGAGAGAAACACTTTCGAGTCCAGAACCCCAAGGAGTGC--- 90
Db 540 TrpCysHisAasp-----LysCysValArgSerGluGluCysLeu 552
Qy 91 -----AAATGGACAGACCCACTCGCTTATAGCGCGCGTGAATAATTTCCAGGTTT 144
Db 553 SerGlyThrTrpThrGlnGlnIleCysLeuProAlaIleTyrLysValPheProAsnSer 572
Qy 145 TTCATGGTTCCGAACAGGTGCTCCGCTGTGTGTCAGCGATGAGAGACCCCAAGCCAGAG 204
Db 573 AlaProLeuGluGly-GlyThrArgLeuThrIleCysGlyTrpAspPheGlyPheArgAr 592
Qy 205 GAGAAGCGGTTTCTCTCTGGAAG 226
Db 592 GAsnAsnLysPheAspLeuLys 599

RESULT 10
US-10-957-351-1
; Sequence 1, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: C-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: C-Met, Hepatocyte Growth Factor/Scatter Factor
; OTHER INFORMATION: (HGF/SF)-binding receptor tyrosine kinase
US-10-957-351-1

Alignment Scores:
Pred. No.:      9.17      Length:      1390
Score:          66.00     Matches:      18
Percent Similarity: 38.2% Conservative: 8
Best Local Similarity: 26.5% Mismatches: 31
Query Match:     13.1% Indels:      11
DB:              6       Gaps:       2

US-10-079-954-2 (1-261) x US-10-957-351-1 (1-1390)

Qy 34 TGGTGTCTATGCTTGTGAGAGAGAAACACTTTCGAGTCCAGAACCCCAAGGAGTGC--- 90
Db 540 TrpCysHisAasp-----LysCysValArgSerGluGluCysLeu 552
Qy 91 -----AAATGGACAGACCCACTCGCTTATAGCGCGCGTGAATAATTTCCAGGTTT 144
Db 553 SerGlyThrTrpThrGlnGlnIleCysLeuProAlaIleTyrLysValPheProAsnSer 572
Qy 145 TTCATGGTTCCGAACAGGTGCTCCGCTGTGTGTCAGCGATGAGAGACCCCAAGCCAGAG 204
Db 573 AlaProLeuGluGly-GlyThrArgLeuThrIleCysGlyTrpAspPheGlyPheArgAr 592
Qy 205 GAGAAGCGGTTTCTCTCTGGAAG 226
Db 592 GAsnAsnLysPheAspLeuLys 599

RESULT 12
US-11-078-735-18
; Sequence 18, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAMARA
```

```
Db 540 TrpCysHisAasp-----LysCysValArgSerGluGluCysLeu 552
Qy 91 -----AAATGGACAGACCCACTCGCTTATAGCGCGCGTGAATAATTTCCAGGTTT 144
Db 553 SerGlyThrTrpThrGlnGlnIleCysLeuProAlaIleTyrLysValPheProAsnSer 572
Qy 145 TTCATGGTTCCGAACAGGTGCTCCGCTGTGTGTCAGCGATGAGAGACCCCAAGCCAGAG 204
Db 573 AlaProLeuGluGly-GlyThrArgLeuThrIleCysGlyTrpAspPheGlyPheArgAr 592
Qy 205 GAGAAGCGGTTTCTCTCTGGAAG 226
Db 592 GAsnAsnLysPheAspLeuLys 599

RESULT 11
US-11-072-175-186
; Sequence 186, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186
; LENGTH: 1408
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-175-186

Alignment Scores:
Pred. No.:      9.17      Length:      1408
Score:          66.00     Matches:      18
Percent Similarity: 38.2% Conservative: 8
Best Local Similarity: 26.5% Mismatches: 31
Query Match:     13.1% Indels:      11
DB:              7       Gaps:       2

US-10-079-954-2 (1-261) x US-11-072-175-186 (1-1408)

Qy 34 TGGTGTCTATGCTTGTGAGAGAGAAACACTTTCGAGTCCAGAACCCCAAGGAGTGC--- 90
Db 540 TrpCysHisAasp-----LysCysValArgSerGluGluCysLeu 552
Qy 91 -----AAATGGACAGACCCACTCGCTTATAGCGCGCGTGAATAATTTCCAGGTTT 144
Db 553 SerGlyThrTrpThrGlnGlnIleCysLeuProAlaIleTyrLysValPheProAsnSer 572
Qy 145 TTCATGGTTCCGAACAGGTGCTCCGCTGTGTGTCAGCGATGAGAGACCCCAAGCCAGAG 204
Db 573 AlaProLeuGluGly-GlyThrArgLeuThrIleCysGlyTrpAspPheGlyPheArgAr 592
Qy 205 GAGAAGCGGTTTCTCTCTGGAAG 226
Db 592 GAsnAsnLysPheAspLeuLys 599

RESULT 12
US-11-078-735-18
; Sequence 18, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAMARA
```

;	TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
:	TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS

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; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-18

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Alignment Scores:	
Pred. No.:	9.89
Score:	65.50
Percent Similarity:	38.8%
Best Local Similarity:	26.2%
Query Match:	13.0%
DB:	7
	Length: 618
	Matches: 27
	Conservative: 14
	Mismatches: 35
	Indels: 27
	Gaps: 7
US-10-079-954-2 (1-261)	x US-11-078-735-18 (1-618)

Qy	13	GACGAGGTGACAAATAGAGTGTGGTGCATGCT---	TGTGAGAGAGAAAACACTTTTCGAG	69
		:::	:::	
Db	212	AspGluCysAlaProLeuValCysArgAlaGlyCysSerProGluHisGlyPhe---	230	
		:::	:::	
Qy	70	TGCCAGAACCCCAAGGAGGTGCAAA-----	TGGACAGAGCCATACTGCGTTATA	117
		:::	:::	
Db	231	CysGluGlnProGlyGluCysArgCysLeuGluGlyTrpThrGlyProLeuCysThrVal	250	
		:::	:::	
Qy	118	-----GCGCGCGTGAATAATTTCCAGT-----	-----TTTTTC	147
		:::	:::	
Db	251	ProValSerThrSerSerCysLeuSerProArgGlyProSerSerAlaThrThrGlyCys	270	
		:::	:::	
Qy	148	ATCGTT-----CGCAACAGGTGCTCCGCTGGTGTGTGCGACGCATG	186	
		:::	:::	
Db	271	LeuValProGlyProGlyProCysAspGlyAsnProCysAlaAanglyGlySerCysSer	290	
		:::	:::	
Qy	187	GAGAGACCCACGACAGAGAGACGGGTTTCTCTGGAGAGCCCATGCCCTTCTTTAC	246	
		:::	:::	
Db	291	GluThrPro-----ArgSerPheGluCysThrCysProArgGlyPheThrGly	306	
		:::	:::	
Qy	247	CTCAAGTGT	255	
		:::	:::	
Db	307	LeuArgCys	309	

RESULT 13
US-11-050-346-63
; Sequence 63, Application US/11050346
; Publication No. US20060002924A1
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA

; APPLICANT: WARD, GEORGE ALBERT
 ; TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND
 ; TITLE OF INVENTION: THEIR USE IN MEDICAL TREATMENT

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/ FILE REFERENCE: 674525-2016
/ CURRENT APPLICATION NUMBER: US/11/050,346
/ CURRENT FILING DATE: 2005-02-03
/ PRIOR APPLICATION NUMBER: GB 0312062.3
/ PRIOR FILING DATE: 2003-05-24
/ PRIOR APPLICATION NUMBER: PCT/GB03/01525
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: GB 0300234.2
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: GB 0218068.5
/ PRIOR FILING DATE: 2002-08-03
/ PRIOR APPLICATION NUMBER: GB 0220849.4
/ PRIOR FILING DATE: 2002-09-07
/ PRIOR APPLICATION NUMBER: GB 0220912.0
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: GB 0220913.8
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: PCT/GB02/05137
/ PRIOR FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: PCT/GB02/05133
/ PRIOR FILING DATE: 2002-11-13
/ NUMBER OF SEQ ID NOS: 69
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 63
/ LENGTH: 618
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-050-346-63

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Alignment Scores:		
Pred. No.:	9.99	Length:
Score:	65.50	Matches:
Percent Similarity:	39.8%	Conservative:
Best Local Similarity:	26.2%	Mismatches:
Query Match:	13.0%	Indels:
DB:	7	Gaps:
		7
US-10-079-954-2 (1-261)	x	US-11-050-346-63 (1-618)

Qy	13	GACGAGGGTGACAAATAGAGTGTGGTGTACGTCT--TGTGAGAGAGAAAACACACTTTCAG	69
Db	212	AspGluCyseGluAlaProLeuValCyseArgAlaGlyCyseProGluHisGlyPhe---	230
Qy	70	TGCAGAACCCAAAGGAGGTGCAAA--TGGACAGAGCCATCTGCGTTATA	117
Db	231	CysGluGlnProGlyGluCyseArgCyseLeuGluGlyTrpThrGlyProLeuCysThrVal	250
Qy	118	-----CGGCGCGTGAANAATATTCACAGT-----TTTTTC	147
Db	251	ProValSerThrSerCysLeuSerProArgGlyProSerSerAlaThrThrGlyCys	270
Qy	148	ATGGT-----CGCAACACAGTGCTCCGCTGGTGTGTCACGCGANG	186
Db	271	LeuValProGlyProGlyProCyseAspGlyAsnProCyseAlaAsnGlyGlySerCysSer	290
Qy	187	GAGAGACCCCAAGCCAGAGGAGACGGGTCTCTCTGGAGAGCCCATGCCCTTCTTTTAT	246
Db	291	GluThrPro-----ArgSerPheGluCysThrCysProArgGlyPheTyrgly	306
Qy	247	CTCAAGTGT	255
Db	307	LeuArgCys	309

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RESULT 14
US-11-103-077-18
; Sequence 18, Application US/11103077
; Publication No. US20060003927A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: YOUNG, LESLEY LYNN

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! TITLE OF INVENTION: MODULATION OF IMMUNE FUNCTION
! FILE REFERENCE: 674525-2020
! CURRENT APPLICATION NUMBER: US/11/103,077
! CURRENT FILING DATE: 2005-04-11
! PRIOR APPLICATION NUMBER: PCT/GB03/04402
! PRIOR FILING DATE: 2003-10-09
! PRIOR APPLICATION NUMBER: GB 0223405.2
! PRIOR FILING DATE: 2002-10-09
! PRIOR APPLICATION NUMBER: GB 0223409.4
! PRIOR FILING DATE: 2002-10-09
! PRIOR APPLICATION NUMBER: GB 0224353.3
! PRIOR FILING DATE: 2002-10-19
! NUMBER OF SEQ ID NOS: 29
! SOFTWARE: PatentIn Ver. 3.3
! SEQ ID NO 18
! LENGTH: 618
! TYPE: PRT
! ORGANISM: Homo sapiens
US-11-103-077-18

Alignment Scores:
Pred. No.: 9 89 Length: 618
Score: 65.50 Matches: 27
Percent Similarity: 39.8% Conservative: 14
Best Local Similarity: 26.2% Mismatches: 35
Query Match: 13.0% Indels: 27
DB: 7 Gaps: 7

US-10-079-954-2 (1-261) x US-11-103-077-18 (1-618)

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QY 13 GACGAGGTGACAATPAGATGTGGTGTGTCATGCT--TGTGAGAGAGAAAAACACTTTTCGAG 69
Db 212 AspGluCysGluAlaProLeuValCysArgAlaGlyCysSerProGluHisGlyPhe---230
QY 70 TGCCAGACCCAGAGAGAGTGCMAA-----TCGACAGACCCATAGTGGTTATA 117
Db 231 CysGluGlnProGlyGluCysArgCysLeuGluGlyTrpThrGlyProLeuCysThrVal 250
QY 118 -----GCGGCGGTGAAAAATATTTCCACGT-----TTTTTC 147
Db 251 ProValSerThrSerSerCysLeuSerProArgGlyProSerSerAlaThrThrGlyCys 270
QY 148 ATGGTT-----CGCAACAGTCTCCGCTGGTGTGTCACGCGATG 186
Db 271 LeuValProGlyProGlyProCysAspGlyAsnProCysAlaAsnGlyGlySerCysSer 290
QY 187 GAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAGAGCCCATGCCCTTTTAC 246
Db 291 GluThrPro-----ArgSerPheGluCysThrCysProArgGlyPheTyrgly 306
QY 247 CTCAGTGT 255
Db 307 LeuArgCys 309
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RESULT 15

US-11-087-099-12253
; Sequence 12253, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12253
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Brassica rapa
US-11-087-099-12253

Alignment Scores:
Pred. No.: 11 Length: 430

Score: 65.00 Matches: 17
Percent Similarity: 46.2% Conservative: 7
Best Local Similarity: 32.7% Mismatches: 22
Query Match: 12.9% Indels: 6
DB: 7 Gaps: 1

US-10-079-954-2 (1-261) x US-11-087-099-12253 (1-430)

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QY 215 AACCGCTTCTCCTCTGCTGGGTCTCTCCATCGTCGACCAACGCGGAGCAGCCTGTG 156
Db 25 AsnThrLeuSerSerThrGluSerLeuThrIleSerSerAsn-----38
QY 155 CGAACCATGAAAAACGTGGAATATTTTCAOGGCCCTATAACGCAGATATGGCTCTGTC 96
Db 39 ArgThrLeuValSerArgGlyAsnValPheGluLeuGlyPheArgThrAsnSerSer 58
QY 95 CATTTGCACCTCTTGGGTTCGCACTCGAAGTG 60
Db 59 SerArgTrpTyrLeuGlyIleTrpTyrLysVal 70
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:46:10 ; Search time 4:77097 Seconds
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Title: US-10-079-954-2

Perfect score: 502

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Maximum Match 100%

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents AA:*
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- /cgn2_6/ptodata/1/iaa/6 COMB pep:*
- /cgn2_6/ptodata/1/iaa/H COMB pep:*
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- /cgn2_6/ptodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.5	19.4	187	2	US-09-949-016-10507
2	75	14.9	159	2	US-09-252-991A-28542
3	73	14.5	136	2	US-09-252-991A-20192
C 4	71.5	14.2	350	2	US-09-248-796A-17746
C 5	71.5	14.2	589	2	US-09-740-041-2
C 6	69	13.7	441	2	US-09-252-991A-18870
C 7	68.5	13.6	559	2	US-09-364-206-47
C 8	68	13.5	1476	2	US-09-817-514A-4
C 9	67.5	13.4	234	2	US-09-270-767-45485
10	67	13.3	598	2	US-08-540-236-3415
11	66.5	13.2	157	2	US-09-252-991A-30532
12	66.5	13.2	178	2	US-09-852-100B-4

C 13	66	13.1	312	2	US-09-188-930-142	Sequence 142, App
C 14	66	13.1	312	2	US-09-312-283C-142	Sequence 142, App
C 15	66	13.1	358	2	US-09-561-077C-64	Sequence 64, Appl
C 16	66	13.1	429	2	US-09-328-352-4392	Sequence 4392, Ap
C 17	66	13.1	469	2	US-09-188-930-339	Sequence 339, App
C 18	66	13.1	469	2	US-09-312-283C-339	Sequence 339, App
C 19	66	13.1	469	2	US-09-991-181-289	Sequence 289, App
C 20	66	13.1	469	2	US-09-990-444-289	Sequence 289, App
C 21	66	13.1	469	2	US-09-997-333-289	Sequence 289, App
C 22	66	13.1	469	2	US-09-992-598-289	Sequence 289, App
C 23	66	13.1	675	1	US-08-386-495-10	Sequence 10, Appl
C 24	66	13.1	675	4	PCT-US96-02331-10	Sequence 10, Appl
C 25	66	13.1	1214	2	US-10-164-595-24	Sequence 24, Appl
C 26	66	13.1	1441	2	US-09-949-016-10397	Sequence 10397, A
C 27	66	13.1	1481	2	US-09-251-645-14	Sequence 14, Appl
C 28	65	12.9	725	2	US-09-234-332-12	Sequence 12, Appl
C 29	65	12.9	842	2	US-09-949-016-8357	Sequence 8357, Ap
C 30	65	12.9	858	2	US-09-538-092-1127	Sequence 1127, Ap
C 31	64.5	12.8	116	2	US-09-973-278-157	Sequence 157, App
C 32	64.5	12.8	117	2	US-09-227-357-238	Sequence 238, App
C 33	64.5	12.8	137	2	US-09-621-976-5741	Sequence 5741, Ap
C 34	64.5	12.8	859	2	US-09-369-364A-5	Sequence 5, Appli
C 35	63.5	12.6	159	6	5208144-35	Patent No. 5208144
C 36	63.5	12.6	182	2	US-09-540-236-3495	Sequence 3495, Ap
C 37	63.5	12.6	208	2	US-09-252-991A-29277	Sequence 29277, A
C 38	63.5	12.6	640	2	US-09-177-165A-30	Sequence 30, Appl
C 39	63	12.5	442	2	US-09-902-540-11579	Sequence 11579, A
C 40	63	12.5	490	2	US-09-270-767-44437	Sequence 44437, A
C 41	62.5	12.5	138	2	US-09-270-767-37396	Sequence 37396, A
C 42	62.5	12.5	188	2	US-09-270-767-52613	Sequence 52613, A
C 43	62.5	12.5	188	2	US-09-252-991A-32431	Sequence 32431, A
C 44	62.5	12.5	536	2	US-09-949-016-10134	Sequence 10134, A
C 45	62.5	12.5	602	2	US-09-252-991A-17752	Sequence 17752, A

ALIGNMENTS

RESULT 1

US-09-949-016-10507
; Sequence 10507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10507
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10507

Alignment Scores:
Pred. No.: 0.000163 Length: 187
Score: 97.50 Matches: 23
Percent Similarity: 46.2% Conservative: 13
Best Local Similarity: 29.5% Mismatches: 35
Query Match: 19.4% Indels: 7
DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x US-09-949-016-10507 (1-187)

Qy 37 TGTCATGCTTTGTGAGAGAGAGAAAACACTTTCAGTGCAGAACCCAGGAGGTGCANATGG 96

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Db      60  CyHieAaspCysAlaValIleAenAaspPheAenCysProAenIleArgValCysProTyr 79
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      97  ACAGAGCCATACATCGGTATAGCGCGGTGAAATATTTCCACGTTTTTTTCATGGTTCG 156
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      80  HisIleArgArgCysMetThrIleSerIleArgIleAenSerArgGluLeuValTyr 99
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      157  AACAGGTGCTCCGCTGGTGT-----GCAGCGATGGAGAGACCAAGCCAGAG 204
      ||| : : : ||| ||||| : : : ||| : : : ||| : : : ||| : : : |||
Db      100  LysAenCysThrAenAenCysThrPheValTyrAlaAlaGluGlnProGluAlaPro 119
      ||| : : : ||| ||||| : : : ||| : : : ||| : : : ||| : : : |||
QY      205  GAGAAGCGGTTTCTCTGGAAGAGCCATGCCCTCTTTTACCTCAAGTGTCT 258
      ||| ||| ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db      120  GlyIysIlePhe-----LysThrAenSerPheTyrTrpValCysCys 134
      ||| ||| ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||

RESULT 2
US-09-252-991A-28542
; Sequence 28542, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28542
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28542

Alignment Scores:
Pred. No.: 0.195 Length: 159
Score: 75.00 Matches: 17
Percent Similarity: 41.8% Conservative: 6
Best Local Similarity: 30.9% Mismatches: 20
Query Match: 14.9% Indels: 12
DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x US-09-252-991A-28542 (1-159)
QY      46  TGTGAGAGAAACACTTTCGAGTCCAGAACCCAGGAGGTGCAATCG----- 96
      ||| ||| : : : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      106  CyThrArgSerSerArgGlyTyrCysValThrProArgAlaCysArgTrpArgThr 125
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      97  ACAGAGCCATACATCGGTATAGCGCGGTGAAATATTTCCACGTTTTTTTCATGGTTCG 156
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      126  SerThrSerArgCysSerProAlaAla-----SerThr 136
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QY      157  AACAGGTGCTCCGCTGGTGTGTGCGAGCGATGGAGAGCCCAAGCCA 201
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      137  SerThrCysArgProGlyCysThrSerMetThrArgProArgPro 151
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RESULT 3
US-09-252-991A-20192
; Sequence 20192, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20192
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20192

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RESULT 6
US-09-252-991A-18870
; Sequence 18870, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A

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QY 214 ACCGTTCTCTGGCTGGTCTCTCCATCGTGCACACGCGGACCTGTTC 155
Db 377 ThrArgSerLeuSerTrpThrProThr-CysThrSerSer----- 391
QY 154 GAACCATGAAAAACGTGGAATATTTTTCAGCGCGCTATACGCGAGTATGGCTCTGTCC 95
Db 392 -----ThrTrpThrCysAlaHisAlaLeuHisProSerThrTrpProCysCy 407
QY 94 ATTGGCACTCTCT----- 82
Db 407 sValAlaProSerSerThrAlaAlaThrProAlaCysArgSerSerCysAlaSerCysSe 427
QY 81 -----TGGGTTCTGGCACTCGAAGTGTCTCTCTCACAAGCATGACACC 35
Db 427 rProSerThrArgTrpLeuAlaAlaAlaArgSerAlaAlaArgAlaAlaSerProSerTh 447
QY 34 ACACCTCTATTGTACC 19
Db 447 rTrpSerThrValThr 452
RESULT 8
US-09-817-514A-4
; Sequence 4, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; PRIORITY FILING DATE: 2000-03-26
; PRIOR FILING DATE: US 60/191806
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1476
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-817-514A-4
Alignment Scores:
Pred. No.: 4.51 Length: 1476
Score: 68.00 Matches: 23
Percent Similarity: 42.9% Conservative: 7
Best Local Similarity: 32.9% Mismatches: 22
Query Match: 13.5% Indels: 18
DB: 2 Gaps: 3
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QY 53 GAGAAACACTTTCAGTGCCAGAACCAAGAGGTGCAATGGACAGACATACGTGC 112
Db 791 GluGlnThrAspSerHisGlnLeuAlaGlnGlyAsnAlaProGluArgThrProProAla 810
QY 113 TTATAGCGCGCTGAAATATATTTCCAGTTTTCATGGTTTCGCAACAGGTGCTCCGCTG 172
Db 811 LeuThrLys-----SerTrpTyrAlaThrGlyLeuProAla 822
QY 173 GTT-----GTGCGCGATGGAGAGACCCCAAGCCAGAGAGAGCGGTTTC 217
Db 823 ValAspAsnAlaLeuSerAlaGlyTyrTrpArgGlyAspLysGlnAlaPheAlaGlyPhe 842
QY 218 TCCTGGAAGAGCCCATGCTCTCTTTTACC 247
Db 843 Thr-----ProArgPheThr 847
RESULT 9
US-09-270-767-45485
; Sequence 45485, Application US/09270767
; Patent No. 6703491
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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45485
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45485
Alignment Scores:
Pred. No.: 2.48 Length: 234
Score: 67.50 Matches: 26
Percent Similarity: 38.5% Conservative: 9
Best Local Similarity: 28.6% Mismatches: 31
Query Match: 13.4% Indels: 25
DB: 2 Gaps: 4
US-10-079-954-2 (1-261) x US-09-270-767-45485 (1-234)
QY 198 CTTGGGTCTCTCCATCGTGC-----ACACGAGCGGACCATCTGTTCG----- 154
Db 133 LeuAsnProLeuHisArgCysGluLeuArgSerThrGluThrProLeuAlaAlaLeuSer 152
QY 153 -----AACCATGAAAAACGTGGAATATTTTTCACGCGCGCTAT 115
Db 153 PheAlaHisThrTyrThrArgThrHisArgLysValIleTyrTyrLeuCysGlyLeuPhe 172
QY 114 AACGCGATGATGGTCTCTCCATTTGCACCTCTCTGGGTTCTGGCAGTTCGAA----- 64
Db 173 TyrLeuThrHisAlaCysValPheAlaProTyrPheIlePheAlaLeuArgIlePheVal 192
QY 63 -----AGTGTTTCTCTCACAAGCATGACACCATCTCTATT--- 25
Db 193 ProLeuValGlyLeuPheSerValLeuLeuValAlaGlnThrSerAspAsnIleGlu 212
QY 24 -----GTCAACCTCGTCCGTTCGCTGGCT 1
Db 213 CysIleAlaValThrAlaSerArgCysIleAla 223
RESULT 10
US-09-540-236-3415
; Sequence 3415, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3415
; LENGTH: 598
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3415
Alignment Scores:
Pred. No.: 4.28 Length: 598
Score: 67.00 Matches: 18
Percent Similarity: 51.5% Conservative: 16
Best Local Similarity: 27.3% Mismatches: 27
Query Match: 13.3% Indels: 5
DB: 2 Gaps: 2
US-10-079-954-2 (1-261) x US-09-540-236-3415 (1-598)
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QY 63 TTTCGAGTCCAGAACCCAGGAGGTGCAATGAGCAGAGCCATACGCTTATAGCGC 122
Db 126 PheLysAlaArgGluWetArgArgileGluGluAlaLysThrValValArgTyrAspPro 145
QY 123 CGTGAATAATTTCCAGCTTTTTCAT-----GTTCCGCAACAGGTGCTCCGC--- 170
Db 146 TyrThrAsnGlnSerThrPheTyrHisArgLeuGluGlyThrAspGluLeuThrVal 165
QY 171 TGGTTGTGACGATGGAGAGACCCAGCCAGGAGGAGCGGTTCTCTGGAAGAGCC 230
Db 166 LysLeuAlaGlnValGlyGluArgGlnValArgAlaMetThrIle-PheLeuLeuAspAs 185
QY 231 CATGCCCTCTTTTAC 246
Db 185 pleuSerTyrPheHis 190

RESULT 11
US-09-252-991A-30532
; Sequence 30532, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30532
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30532

Alignment Scores:
Pred. No.: 2.89 Length: 157
Score: 66.50 Matches: 29
Percent Similarity: 37.6% Conservative: 6
Best Local Similarity: 31.2% Mismatches: 42
Query Match: 13.2% Indels: 16
DB: 2 Gaps: 4

US-10-079-954-2 (1-261) x US-09-252-991A-30532 (1-157)
QY 1 AGCCAGCGAACCGACGAGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAAC 60
Db 48 SerProArgSerProGluProCysSerArgProTrpCysProAlaCysAlaSerAlaAsn 67
QY 61 ACTTTCGAGTCCAGAACCCAGGAGGTGCAATGAGCAGAGCCATACGCTTATAGCG 120
Db 68 SerAlaSerCysAlaIleProThrArgAla---TyrArg-----TyrSerProArgSer 84
QY 121 GCCGTGAATAATTTCCAGCTTTTTCATGTTGTCGAAC---AGTGTGCTCC----- 168
Db 85 SerAlaSerSerSerThrArgArgCysSerProArgSerAlaArgCysSerGlyPhePro 104
QY 169 -----GCTGTTGTGACGCGATGGAGAGCCAGCCAGCCAGCCAGCAG 204
Db 105 ProThrProLysSerAlaLeuProAlaAlaCysIleAla-TyrArgLeuAlaSerThrCy 124
QY 205 GAGAGCGGTTCTCTCGAAGAGCCAGCCAGCCCTTCT 241
Db 124 sSerGlyArgCysSerThrAlaSerAlaAlaProSer 136

RESULT 12
US-09-852-100B-4
; Sequence 4, Application US/09852100B
; Patent No. 6787319

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Ozenberger, Bradley A.
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Kajkowski, Eileen M.
; APPLICANT: Jacobsen, Jack S.
; APPLICANT: Walker, Stephen G.
; APPLICANT: Sophia, Heidi
; APPLICANT: Howland, David
; TITLE OF INVENTION: Beta-Amyloid Peptide-Binding Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 31896-67200 (AHP98126 P2)
; CURRENT APPLICATION NUMBER: US/09/852,100B
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/774,936
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/21621
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/172,990
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: US 60/104,104
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/060,609
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: US 60/064,583
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-852-100B-4

Alignment Scores:
Pred. No.: 3.05 Length: 178
Score: 66.50 Matches: 16
Percent Similarity: 42.1% Conservative: 0
Best Local Similarity: 42.1% Mismatches: 17
Query Match: 13.2% Indels: 5
DB: 2 Gaps: 1

US-10-079-954-2 (1-261) x US-09-852-100B-4 (1-178)
QY 10 ACGACGAGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACACCTTCGAG 69
Db 53 ThrArgGluGlyArgAlaArgValTrpCysIleAlaAlaAlaGluIleAsnCyThrGlu 72
QY 70 TGCCAGAACCCAGG-----AGGTGCAATGAGCAGAGCCATAC 108
Db 73 ThrGlyAsnAlaThrPheThrArgGluValProCysLysTrpThrAsnGlyTyr 90

RESULT 13
US-09-188-930-142
; Sequence 142, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Muirson, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.101C1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 142
; LENGTH: 312
; TYPE: PRT
; ORGANISM: mouse

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:49:19 ; Search time 2.44839 Seconds
(without alignments)
694.416 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 159630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 339260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications AA New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	80.3	241	7	US-11-019-711-77 Sequence 77, Appl
2	453	80.3	241	7	US-11-019-711-78 Sequence 78, Appl
3	453	80.3	241	7	US-11-234-786-114 Sequence 114, Appl
4	371	65.8	240	7	US-11-019-711-76 Sequence 76, Appl
5	358	63.5	126	5	US-09-978-360A-555 Sequence 555, Appl
6	357.5	63.4	241	7	US-11-019-711-22 Sequence 22, Appl
7	172.5	30.6	222	7	US-11-019-711-81 Sequence 81, Appl
8	158	28.0	247	7	US-11-019-711-79 Sequence 79, Appl
9	137.5	24.4	237	7	US-11-108-172-1062 Sequence 1062, Ap

Sequence 1122, Ap
Sequence 1085, Ap
Sequence 1121, Ap
Sequence 248, Appl
Sequence 6, Appl
Sequence 1266, Ap
Sequence 80, Appl
Sequence 20, Appl
Sequence 25, Appl
Sequence 1686, Ap
Sequence 482, App
Sequence 464, App
Sequence 860, App
Sequence 108, Appl
Sequence 23452, A
Sequence 23451, A
Sequence 23450, A
Sequence 1116, Ap
Sequence 63, Appl
Sequence 23765, A
Sequence 2456, Ap
Sequence 23201, A
Sequence 19585, A
Sequence 16703, A
Sequence 16702, A
Sequence 16701, A
Sequence 27, Appl
Sequence 10091, A
Sequence 19503, A
Sequence 10159, A
Sequence 19501, A
Sequence 23, Appl
Sequence 2, Appl
Sequence 9456, Ap
Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-11-019-711-77
; Sequence 77, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kikuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Eisinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eissen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235

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; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-711-77

Alignment Scores:
Pred. No.: 1 38e-39 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 7 Gaps: 0

US-10-079-954-1 (1-297) x US-11-019-711-77 (1-241)

Qy 1 GCAATCGATGGGCACTCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAG 60
Db 33 SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52
Qy 61 TTGTCAACGTGGGCTACTTCTCTATCCACCGCGGTGTGCTTCTTGGTTTC 120
Db 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
Qy 121 CTGGCTGCTATGCTGCTAGACTGAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
Qy 181 CTCCTCCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValThrThr 112
Qy 241 ATGGCTGAGCACTTCCCGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 2
US-11-019-711-78
; Sequence 78, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alcobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M

; APPLICANT: Burgees, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-711-78

Alignment Scores:
Pred. No.: 1 38e-39 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 7 Gaps: 0

US-10-079-954-1 (1-297) x US-11-019-711-78 (1-241)

Qy 1 GCAATCGATGGGCACTCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAG 60
Db 33 SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52
Qy 61 TTGTCAACGTGGGCTACTTCTCTATCCACCGCGGTGTGCTTCTTGGTTTC 120
Db 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
Qy 121 CTGGCTGCTATGCTGCTAGACTGAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
Qy 181 CTCCTCCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValThrThr 112
Qy 241 ATGGCTGAGCACTTCCCGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128
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; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 76
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-019-711-76

Alignment Scores:
Pred. No.: 4.75e-31 Length: 240
Score: 371.00 Matches: 73
Percent Similarity: 87.5% Conservative: 11
Best Local Similarity: 76.0% Mismatches: 12
Query Match: 65.8% Indels: 0
DB: 7 Gaps: 0

US-10-079-954-1 (1-297) x US-11-019-711-76 (1-240)

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Db 33 SerValaAspGlyThrSerPheLeuLysValPheGlySerLeuSerSerAlaMetGln 52
Qy 61 TTTGTCAAGTGGGCTACTTCTCATCGACCGCGCTTGGGCTTGTGCTTCTTGGTTTC 120
Db 53 PheValaAsnValGlyThrPheLeuLysValPheGlySerLeuLysValPheGlyPhe 72
Qy 121 CTGGGCTGCTATGCTGCTAGACTGAGACGAGCAAGTGTGCCCTCGACGCTTCTTCTCATC 180
Db 73 LeuGlyCysTyrGlyAlaHisSerGluAenLysCysValLeuMetMetPhePheSerIle 92
Qy 181 CTCCTCTCATCTTCATGCTGAGTTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 93 LeuLeuIleIlePheIleAlaGluIleAlaGlyAlaValValAlaLeuValTyrThr 112
Qy 241 ATGGCTGAGCACTTCCGACGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
Db 113 LeuAlaGluGlnPheLeuThrLeuLeuValValProAlaIleGluLys 128

RESULT 5
US-09-978-360A-555
; Sequence 555, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.USA.CIP
; CURRENT APPLICATION NUMBER: US/09/978.360A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 555
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -27..-1
US-09-978-360A-555

Alignment Scores:
Pred. No.: 1.05e-29 Length: 126
Score: 358.00 Matches: 74
Percent Similarity: 94.9% Conservative: 0
Best Local Similarity: 94.9% Mismatches: 4
Query Match: 63.5% Indels: 0
DB: 5 Gaps: 0

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Qy 55 ATGCAGTTTGTCAACGTGGGCTACTTCTCATCCAGCCGCGCTGTGGTCTTTGCTCTT 114
Db 1 MetGlnPheValaAsnValGlyThrPheLeuLysValPheGlySerLeuLysValPheGlyPhe 20
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Db 21 GlyPheLeuGlyCysTyrGlyAlaLysThrGluSerMetCysAlaLeuValThrPhePhe 40
Qy 175 TTCATCTCTCTCTCATCTTCTTCTGCTGAGTTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCT 234
Db 41 PheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
Qy 235 ACCAATATGCTGAGCACTTCCGACGCTTCCGACGCTTCCGACGCTTCCGACGCTTCCGACGAG 288
Db 61 ThrThrMetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 78

RESULT 6
US-11-019-711-22
; Sequence 22, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21

```

US-10-079-954-1 (1-297) x US-11-019-711-81 (1-222)

Qy	4	ATCGATGGGGCATCTCTTCTGAAGATCTTGGGGCCACTGTCGCCAGTGCATGCAGTTT	63
Db	27	ValAspLeuSerSerPheSerGluLeuLeuGlySerLeuSerSer-----	41
Qy	64	GTCAACGGGGCTACTTCTCATCGACGGGGTGTGTGTCTTGCTTTGTTGTTTCCCTG	123
Db	42	LeuValAlaAlaTyrrValLeuAlaValGlyAlaIleLeuPheLeuValGlyPheLeu	61
Qy	124	GGCTGCTATGTGTGAAGACTGACAGCAAGTGGCCCTCGTACGTTCTTCTTTCATCCTC	183
Db	62	GlyCysCysGlyAlaIleArgGluSerArgCysLeuLeuGlyLeuTyrrPheValPheLeu	81

Qy 184 CTCCTCATCTTCATTGCTGAGGTTCACAGTCTGCTGGTGGCTGGTGTAC 234
Db 82 LeuLeuIlePheIleLeuGluValAlaAlaGlyIleLeuAlaPheValPhe 98

RESULT 8

US-11-019-711-79
; Sequence 79, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-019-711-79

Alignment Scores:
Pred. No.: 7.17e-09 Length: 247
Score: 158.00 Matches: 31
Percent Similarity: 67.5% Conservative: 21
Best Local Similarity: 40.3% Mismatches: 21
Query Match: Indels: 4

DB: 7 Gaps: 2
US-10-079-954-1 (1-297) x US-11-019-711-79 (1-247)
Qy 4 ATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGCCAGTCGACGATTT 63
Db 36 ValAspProThrGlyPheArgGluIle-----ValAlaAlaAsnProLeuLeuPhe 52
Qy 64 GTCACGTGGGCTACTTCCTCATCGACGCCGGGTGGTGGTCTTGGTTCCTG 123
Db 53 ThrGly---AlaTyrIleMetLeuAlaMetGlyAlaMetLeuLeuGlyPheLeu 71
Qy 124 GGTCGTATGCTGTAAGACTGAGACCAAGTGGCCCTCGTGAGTCTCTTCATCCTC 183
Db 72 GlyCysGlyAlaIleArgGluAsnLysCysLeuLeuLeuPhePheMetPheIle 91
Qy 184 CTCCTCATCTTCATTGCTGAGGTTCACAGTCTGCTGGTGGCTGGTGTAC 234
Db 92 LeuLeuIlePheLeuAlaGluLeuSerAlaAlaIleLeuAlaPheIlePhe 108

RESULT 9

US-11-108-172-1062
; Sequence 1062, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Cartier, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121-471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1062
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-108-172-1062

Alignment Scores:
 Pred. No.: 9, 75e-07 Length: 237
 Score: 137.50 Matches: 30
 Percent Similarity: 59.4% Conservatives: 11
 Best Local Similarity: 43.5% Mismatches: 27
 Query Match: 24.4% Indels: 1
 Gaps: 1

US-10-079-954-1 (1-297) x US-11-108-172-1062 (1-237)

Qy 28 ATCTTCGGCCACTGTCCTCCAGTGCATGCTTGTCAACGTGGCTACTTCTCTCATC 87
 ||||| ||||| : : : : : |||||
 Db 42 IlephedglySerGluaspValglySerSerTyrValAlaValasp---Ileleulle 60
 ||||| ||||| : : : : : |||||
 Qy 88 GCAGCGCGGTGGCTTTGCTTGTCTTCTTCTGGCTGCTATGGTGAAGACTGAG 147
 ||||| ||||| : : : : : |||||
 Db 61 AlaValGlyAlaIlelleMetIleLeuGlyCysCysGlyAlaIleLysGlu 80
 ||||| ||||| : : : : : |||||
 Qy 148 AGCAAGTGTGCTGCTGCTGCTTCTTCTCATCTCTCTCTCATCTTCTGCTGAGTT 207
 ||||| ||||| : : : : : |||||
 Db 81 SerArgCysMetLeuLeuPhePheIleGlyLeuLeuLeuLeuLeuGlnVal 100
 ||||| ||||| : : : : : |||||
 Qy 208 GCAGCTGCTGTGGTGGCTTGTGTATC 234
 ||||| ||||| : : : : : |||||
 Db 101 AlathrGlyIleLeuGlyAlaValPhe 109
 ||||| ||||| : : : : : |||||

RESULT 10

US-11-108-172-1122
 ; Sequence 1122, Application US/11108172
 ; Publication No. US20050260177A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Jiang, Yudi
 ; APPLICANT: Smith, Carole L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Skeiky, Yasir A. W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick Thomas S.
 ; APPLICANT: Carter, Darrick
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.471C15
 ; CURRENT APPLICATION NUMBER: US/11/108,172
 ; CURRENT FILING DATE: 2005-04-15
 ; PRIOR APPLICATION NUMBER: US 10/025,380
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: US 09/922,217
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 09/833,263
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: US 09/649,448
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 09/575,251
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 09/519,444
 ; PRIOR FILING DATE: 2000-03-06
 ; PRIOR APPLICATION NUMBER: US 09/504,629
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: US 09/480,321
 ; PRIOR FILING DATE: 2000-01-10
 ; PRIOR APPLICATION NUMBER: US 09/476,296

PRIOR FILING DATE: 1999-12-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1130
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1122
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-108-172-1122

Alignment Scores:

Pred. No.: 9, 76e-07 Length: 243
 Score: 137.50 Matches: 30
 Percent Similarity: 59.4% Conservatives: 11
 Best Local Similarity: 43.5% Mismatches: 27
 Query Match: 24.4% Indels: 1
 Gaps: 1

US-10-079-954-1 (1-297) x US-11-108-172-1122 (1-243)

Qy 28 ATCTTCGGCCACTGTCCTCCAGTGCATGCTTGTCAACGTGGCTACTTCTCTCATC 87
 ||||| ||||| : : : : : |||||
 Db 42 IlephedglySerGluaspValglySerSerTyrValAlaValasp---Ileleulle 60
 ||||| ||||| : : : : : |||||
 Qy 88 GCAGCGCGGTGGCTTTGCTTGTCTTGTCTTCTGGCTGCTATGGTGAAGACTGAG 147
 ||||| ||||| : : : : : |||||
 Db 61 AlaValGlyAlaIlelleMetIleLeuGlyCysCysGlyAlaIleLysGlu 80
 ||||| ||||| : : : : : |||||
 Qy 148 AGCAAGTGTGCTGCTGCTGCTTCTTCTCATCTCTCTCTCATCTTCTGCTGAGTT 207
 ||||| ||||| : : : : : |||||
 Db 81 SerArgCysMetLeuLeuPhePheIleGlyLeuLeuLeuLeuLeuGlnVal 100
 ||||| ||||| : : : : : |||||
 Qy 208 GCAGCTGCTGTGGTGGCTTGTGTATC 234
 ||||| ||||| : : : : : |||||
 Db 101 AlathrGlyIleLeuGlyAlaValPhe 109
 ||||| ||||| : : : : : |||||

RESULT 11

US-11-108-172-1085
 ; Sequence 1085, Application US/11108172
 ; Publication No. US20050260177A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Jiang, Yudi
 ; APPLICANT: Smith, Carole L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Skeiky, Yasir A. W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick Thomas S.
 ; APPLICANT: Carter, Darrick
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.471C15
 ; CURRENT APPLICATION NUMBER: US/11/108,172
 ; CURRENT FILING DATE: 2005-04-15
 ; PRIOR APPLICATION NUMBER: US 10/025,380
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: US 09/922,217
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 09/833,263
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: US 09/649,811
 ; PRIOR FILING DATE: 2000-08-28
 ; PRIOR APPLICATION NUMBER: US 09/609,448
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 09/575,251

```
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1085
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1085

Alignment Scores:
Pred. No.: 9.9e-07 Length: 344
Score: 137.50 Matches: 30
Percent Similarity: 59.4% Conservative: 11
Best Local Similarity: 43.5% Mismatches: 27
Query Match: 24.4% Indels: 1
DB: 7 Gaps: 1

US-10-079-954-1 (1-297) x US-11-108-172-1085 (1-344)
Qy 28 ATCTTCGGGCGCAGTGTCTCCAGTCCAGTGTTCACAGTGGGCTACTTCTCATC 87
Db 149 lIePheGlySerGluaspValGlySerSerTyrrValAlaValasp---lIeLeuIle 167
Qy 88 GCAGCCGCGTGTGGTCTTTGCTCTTGGTTCCTGGGCTGCTATGGTGAAGACTGAG 147
Db 168 AlaValGlyAlaIleMetIleLeuGlyPheLeuGlyCysGlyAlaIleLysGlu 187
Qy 148 AGCAAGTGTGCGCTTCAGTCTTCTTCATCTCCTCCCTCATCTTCATGCTGAGGTT 207
Db 188 SerArgCysMetLeuLeuPhePheIleGlyLeuLeuIleLeuLeuGlnVal 207
Qy 208 GCAGCTGCTGTGGTGGCTTGTGTGTAC 234
Db 208 AlaThrGlyIleLeuGlyAlaValPhe 216

RESULT 12
US-11-108-172-1121
; Sequence 1121, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Fongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; CURRENT APPLICATION NUMBER: US/11108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
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; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1121
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1121

Alignment Scores:
Pred. No.: 1e-06 Length: 446
Score: 137.50 Matches: 30
Percent Similarity: 59.4% Conservative: 11
Best Local Similarity: 43.5% Mismatches: 27
Query Match: 24.4% Indels: 1
DB: 7 Gaps: 1

US-10-079-954-1 (1-297) x US-11-108-172-1121 (1-446)
Qy 28 ATCTTCGGGCGCAGTGTCTCCAGTCCAGTGTTCACAGTGGGCTACTTCTCATC 87
Db 245 lIePheGlySerGluaspValGlySerSerTyrrValAlaValasp---lIeLeuIle 263
Qy 88 GCAGCCGCGTGTGGTCTTTGCTCTTGGTTCCTGGGCTGCTATGGTGAAGACTGAG 147
Db 264 AlaValGlyAlaIleMetIleLeuGlyPheLeuGlyCysGlyAlaIleLysGlu 283
Qy 148 AGCAAGTGTGCGCTTCAGTCTTCTTCATCTCCTCCCTCATCTTCATGCTGAGGTT 207
Db 284 SerArgCysMetLeuLeuPhePheIleGlyLeuLeuIleLeuLeuGlnVal 303
Qy 208 GCAGCTGCTGTGGTGGCTTGTGTGTAC 234
Db 304 AlaThrGlyIleLeuGlyAlaValPhe 312

RESULT 13
US-10-501-035-248
; Sequence 248, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 248
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-248
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Alignment Scores:		
Pred. No.:	4.64e-06	253
Score:	131.00	24
Percent Similarity:	59.6%	Conservative: 10
Best Local Similarity:	42.1%	Mismatches: 23
Query Match:	23.2%	Indels: 0
DB:	6	Gaps: 0

US-10-079-954-1 (1-297) x US-10-501-035-248 (1-253)

82	CTC	ATC	GC	AG	CG	CGG	CTT	GGT	CTT	TCT	CTT	GGT	TCT	CGG	CTG	TAA	GGT	CT	TAAG	141	
	:::						:::					:::									
57	lle	lle	Ala	Val	Gly	Ala	Leu	Phe	lle	lle	Gly	Leu	lle	Gly	Cys	Cys	Ala	Thr	lle	76	
	:::						:::					:::									
142	ACT	G	A	G	A	G	A	G	T	G	C	C	T	G	T	G	A	G	T	201	
	:::						:::					:::									
77	Arg	G	l	u	s	r	Arg	C	ys	G	l	y	L	eu	A	l	a	l	a	Thr	96
	:::						:::					:::									
202	G	A	G	T	T	G	C	A	G	T	G	T	G	T	G	C	T	T	G	252	
	:::						:::					:::									
97	Glu	U	Val	Val	Val	Val	Leu	Gly	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	113		
	:::						:::					:::									

RESULT 14

US-11-029-188-6
; Sequence 6, Application US/11029188
; Publication No. US20060013832A1
; GENERAL INFORMATION:
; APPLICANT: JUNE, CARL H.
; APPLICANT: THOMPSON, CRAIG B.
; APPLICANT: NABEL, GARY J.
; APPLICANT: GRAY, GARY S.
; APPLICANT: RENNERT, PAUL D.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING PROLIFERATION OF T
; TITLE OF INVENTION: CELLS

```

FILE REFERENCE: 36119-125 US13
CURRENT APPLICATION NUMBER: US/11/029,188
CURRENT FILING DATE: 2005-01-04
PRIORITY APPLICATION NUMBER: 08/592,711
PRIORITY FILING DATE: 1996-01-26
PRIORITY APPLICATION NUMBER: 08/435,816
PRIORITY FILING DATE: 1995-05-04
PRIORITY APPLICATION NUMBER: 08/403,253
PRIORITY FILING DATE: 1995-03-10
PRIORITY APPLICATION NUMBER: 08/253,964
PRIORITY FILING DATE: 1994-06-03
PRIORITY APPLICATION NUMBER: 08/073,223
PRIORITY FILING DATE: 1993-06-04
PRIORITY APPLICATION NUMBER: 07/864,866
PRIORITY FILING DATE: 1992-04-07
PRIORITY APPLICATION NUMBER: 07/864,807
PRIORITY FILING DATE: 1992-04-07
PRIORITY APPLICATION NUMBER: 07/864,805
PRIORITY FILING DATE: 1992-04-07
PRIORITY APPLICATION NUMBER: 07/275,433
PRIORITY FILING DATE: 1988-11-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 6

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Alignment Scores:	5.88e-06	Length:	227
Pred. No.:	130.00	Matches:	26
Score:	68.8%	Conservative:	7
Percent Similarity:	54.2%	Mismatches:	15
Best Local Similarity:	23.0%	Indels:	0
Query Match:	7	Gaps:	0
DB:			

US-10-079-954-1 (1-297) x US-11-029-188-6 (1-227)

[illegible]

RESULT 15

```

US-10-821-234-1266
: Sequence 1266, Application US/10821234
: Publication No. US20050255114A1
: GENERAL INFORMATION:
: APPLICANT: Labat, Ivan
: APPLICANT: Stache-Crain, Birgit
: APPLICANT: Andarmani, Susan
: APPLICANT: Tang, Y. Tom
: TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclerlampia
: FILE REFERENCE: 821A

```

Alignment Scores:	5.89e-06	Length:	228
Pred. No.:	Score:	Matches:	26
	130.00	Conservative:	7
	68.8%	Mismatches:	15
Best Local Similarity:	54.2%	Indels:	0
Query Match:	23.0%	Gaps:	0
DB:	6		

US-10-079-954-1 (1-297) x US-10-821-234-1266 (1-228)

Qy	76	TACTTCCTCATCGACGCCGGTGTGCTTTGCTCTTGTTTCCTGGCGCTGCTAGGT	135
		:::: :::::	
Db	61	TyrIleIeuIleIGlyAlaGlyAlaLeuMetMetLeuValGlyPheLeuGlyCysCysgly	80
Qy	136	GCTAAGACTGAGAGCAAGTGTGCCTCGTGACGGTCTCTTCATCCCTCCTCATCTTC	195
		:::::	
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Search completed: March 23, 2006, 12:55:35
Job time : 14.2419 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:47:34 ; Search time 17.8839 Seconds
(without alignments)
1387.790 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA_Main:

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	453	80.3	233	3	US-09-148-545-137
3	453	80.3	233	5	US-10-979-111-137
4	453	80.3	241	3	US-09-759-143-114
5	453	80.3	241	3	US-09-780-669-114
6	453	80.3	241	3	US-09-030-606-114
7	453	80.3	241	3	US-09-822-827-114
8	453	80.3	241	3	US-09-115-453-114
9	453	80.3	241	3	US-09-232-880-114
10	453	80.3	241	3	US-09-908-193-44
11	453	80.3	241	3	US-09-895-793-114

12	453	80.3	241	3	US-09-895-814-114	Sequence 114, App
13	453	80.3	241	4	US-10-012-896-114	Sequence 114, App
14	453	80.3	241	4	US-10-097-340-326	Sequence 326, App
15	453	80.3	241	4	US-10-010-940-114	Sequence 114, App
16	453	80.3	241	4	US-10-205-823-425	Sequence 425, App
17	453	80.3	241	4	US-10-144-678A-114	Sequence 114, App
18	453	80.3	241	4	US-10-294-025-114	Sequence 604, App
19	453	80.3	241	4	US-10-295-027-604	Sequence 77, Appl
20	453	80.3	241	4	US-10-037-417-77	Sequence 78, Appl
21	453	80.3	241	4	US-10-037-417-77	Sequence 114, App
22	453	80.3	241	4	US-10-688-838-114	Sequence 425, App
23	453	80.3	241	6	US-11-051-454-425	Sequence 326, App
24	453	80.3	241	6	US-11-050-926-326	Sequence 324, App
25	453	80.3	258	4	US-10-097-340-324	Sequence 423, App
26	453	80.3	258	4	US-10-205-823-423	Sequence 423, App
27	453	80.3	258	6	US-11-051-454-423	Sequence 324, App
28	453	80.3	258	6	US-11-050-926-324	Sequence 20, Appl
29	453	80.3	273	4	US-10-156-136-20	Sequence 1489, Ap
30	453	80.3	273	6	US-11-041-419-20	Sequence 20, Appl
31	436.5	77.4	240	4	US-10-264-237-1489	Sequence 4346, Ap
32	401	71.1	121	4	US-10-264-049-4346	Sequence 43, Appl
33	371	65.8	240	3	US-09-908-193-43	Sequence 74, Appl
34	371	65.8	240	3	US-09-823-187-74	Sequence 76, Appl
35	371	65.8	240	4	US-10-037-417-76	Sequence 3062, Ap
36	365	64.7	103	3	US-09-864-408A-3062	Sequence 555, App
37	358	63.5	126	3	US-09-978-360A-555	Sequence 22, Appl
38	357.5	63.4	241	4	US-10-037-417-22	Sequence 6493, Ap
39	250	44.3	96	4	US-10-106-698-6493	Sequence 19, Appl
40	180	31.9	172	5	US-10-495-148-19	Sequence 81, Appl
41	172.5	30.6	222	4	US-10-037-417-81	Sequence 39, Appl
42	167.5	29.7	166	3	US-09-976-782-39	Sequence 76, Appl
43	165.5	29.3	157	3	US-09-823-187-76	Sequence 42, Appl
44	158	28.0	247	3	US-09-908-193-42	Sequence 72, Appl
45	158	28.0	247	3	US-09-823-187-72	

ALIGNMENTS

RESULT 1

US-09-981-876-137
; Sequence 137, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
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; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
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; PRIOR APPLICATION NUMBER: 60/040,336
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; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502

;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,909
;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR APPLICATION NUMBER: 60/056,862
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,908
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/048,964
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/057,650
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/056,884
;; PRIOR FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 280
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 137
;; LENGTH: 233

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Pred. No.: 3.33e-40 Length: 233
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 3 Gaps: 0

US-10-079-954-1 (1-297) x US-09-981-876-137 (1-233)

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DB 64 LeuGlyCysTyGlyAlaYsThrGluSerTySCysAlaLeuValThrPhePhePhe 83
QY 181 CTCCTCTCATCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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QY 241 ATGCTGAGCAGCTTCCGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
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RESULT 2

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; Sequence 137, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/048,974
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

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Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
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Db 64 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheile 83
Qy 181 CTCTCTCTCATCTTCATTCGCTGAGGTTGAGCTGCTGTGTGCTGCTGCTGTGTACACATA 240
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Qy 241 ATGGCTGAGCACCTCCGACGTTGCTGCTAGTGCCTGCCATCAAGAG 288
Db 104 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 119

RESULT 3

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; Sequence 137, Application US/10979111
; Publication No. US20050215775A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins


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; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-114

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Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
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RESULT 6
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; Sequence 114, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCE: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-114

Alignment Scores:
Pred. No.: 3.35e-40 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 3 Gaps: 0

US-10-079-954-1 (1-297) x US-09-030-606-114 (1-241)
Qy 1 GCATCGATGGGCGATCCCTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCGAG 60
Db ::::
33 SerileAspGlyAlaSerPheLeuIlePheGlyProLeuSerSerAlaMetGln 52
Qy 61 TTGTGCAACGTGGGCTACTTCTCATCGACGCGCGTGTGCTTGTGCTTGTGCTTTC 120
Db 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
Qy 121 CTGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGCAGCTTCTTCTCATC 180
Db 73 LeuGlyCysTyrGlyAlaIleThrGluSerLysCysAlaLeuValThrPhePhePhele 92
Qy 181 CTCCTCTCATCTCATCTGCTGAGTTGCGAGTGTGCTGCGCTTGTGCTGCTACACCAT 240
Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaValAlaLeuValTyrThr 112
Qy 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 288
Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 7
US-09-822-827-114
; Sequence 114, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-114

Alignment Scores:
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Pred. No.: 3.35e-40 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 3 Gaps: 0

US-10-079-954-1 (1-297) x US-09-822-827-114 (1-241)

QY 1 GCAATCGATGGGACATCTTCTGAGATCTTCGGGCGACATGCTGCAGTGCATGCAG 60
DB 33 SerileaspGlyAlaSerPheLeuValPheGlyProLeuSerSerAlaMetGln 52
QY 61 TTGTCAACGGGCTACTTCTCATCGACCGCGGTGTGGTCTTTGCTCTTGGTTTC 120
DB 53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGGCTGCTATGCTAGACGAGAGAGAGTGCCTCGGAGCTTCTTCTTCATC 180
DB 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhe 92
QY 181 CTCTCTCATCTTCATCTGAGGTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 93 LeuLeuLeuLeuPheIleAlaGluValAlaAlaValAlaLeuValTyrThr 112
QY 241 ATGGCTGAGCAGCTTCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
DB 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 8
US-09-115-453-114
; Sequence 114, Application US/09115453B
; Patent No. US2002090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-115-453-114

Alignment Scores:
Pred. No.: 3.35e-40 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 3 Gaps: 0

US-10-079-954-1 (1-297) x US-09-115-453-114 (1-241)

QY 1 GCAATCGATGGGACATCTTCTGAGATCTTCGGGCGACATGCTGCAGTGCATGCAG 60
DB 33 SerileaspGlyAlaSerPheLeuValPheGlyProLeuSerSerAlaMetGln 52
QY 61 TTGTCAACGGGCTACTTCTCATCGACCGCGGTGTGGTCTTTGCTCTTGGTTTC 120
DB 53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGGCTGCTATGCTAGACGAGAGAGTGCCTCGGAGCTTCTTCTTCATC 180
DB 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhe 92
QY 181 CTCTCTCATCTTCATCTGAGGTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 93 LeuLeuLeuLeuPheIleAlaGluValAlaAlaValAlaLeuValTyrThr 112
QY 241 ATGGCTGAGCAGCTTCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
DB 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 9
US-09-232-880-114
; Sequence 114, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-232-880-114

Alignment Scores:
Pred. No.: 3.35e-40 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 3 Gaps: 0

US-10-079-954-1 (1-297) x US-09-232-880-114 (1-241)

QY 1 GCAATCGATGGGACATCTTCTGAGATCTTCGGGCGACATGCTGCAGTGCATGCAG 60
DB 33 SerileaspGlyAlaSerPheLeuValPheGlyProLeuSerSerAlaMetGln 52
QY 61 TTGTCAACGGGCTACTTCTCATCGACCGCGGTGTGGTCTTTGCTCTTGGTTTC 120
DB 53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGGCTGCTATGCTAGACGAGAGAGTGCCTCGGAGCTTCTTCTTCATC 180
DB 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhe 92
QY 181 CTCTCTCATCTTCATCTGAGGTTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 93 LeuLeuLeuLeuPheIleAlaGluValAlaAlaValAlaLeuValTyrThr 112
QY 241 ATGGCTGAGCAGCTTCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
DB 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 10
US-09-908-193-44
; Sequence 44, Application US/09908193
; Publication No. US20020192748A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; APPLICANT: SHIMKETS, RICHARD A.
; APPLICANT: ZERHUSEN, BRYAN
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: PADICARU, MURALIDHARA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 21402-062
; CURRENT APPLICATION NUMBER: US/09/908,193
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/220,273
; PRIOR FILING DATE: 2000-07-24
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:29:14 ; Search time 21.929 Seconds

(without alignments)
1190.162 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USFR=US1007954 @CGN 1 1 476 @runat_23032006_102927_1781 -NCPUs=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A Geneseq 21.*
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2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	85.8	99	2 AAW47275	AAW47275 Human HPK
2	453	80.3	214	8 ADR65994	ADR65994 Human pro
3	453	80.3	214	8 ADR66892	ADR66892 Human pro
4	453	80.3	233	2 AAW75060	AAW75060 Human sec
5	453	80.3	233	6 ABO01936	ABO01936 Novel hum
6	453	80.3	233	9 ADZ12337	ADZ12337 Human sec
7	453	80.3	240	4 AAG62153	AAG62153 Human P50
8	453	80.3	241	2 AAW69386	AAW69386 Prostate
9	453	80.3	241	2 AAW59954	AAW59954 Amino aci

10	453	80.3	241	2 AAW71870	AAW71870 Amino aci
11	453	80.3	241	2 AAW58380	AAW58380 Human sec
12	453	80.3	241	3 AAY82003	AAY82003 Human imm
13	453	80.3	241	3 ABG94412	ABG94412 Human pro
14	453	80.3	241	4 AAM01118	AAM01118 Human pro
15	453	80.3	241	4 AAU69764	AAU69764 Human pro
16	453	80.3	241	4 AAB74801	AAB74801 Prostate
17	453	80.3	241	4 AAG99003	AAG99003 Human pro
18	453	80.3	241	4 ABU71654	ABU71654 Prostate
19	453	80.3	241	4 AAB90679	AAB90679 Human AR4
20	453	80.3	241	4 AAU04982	AAU04982 Human pro
21	453	80.3	241	5 ABG96434	ABG96434 Human ova
22	453	80.3	241	5 ABB95223	ABB95223 Human N1-
23	453	80.3	241	5 ABG76666	ABG76666 Prostate
24	453	80.3	241	6 ABR54335	ABR54335 Prostate
25	453	80.3	241	7 ADB75601	ADB75601 Prostate
26	453	80.3	241	7 ADB13584	ADB13584 Human pro
27	453	80.3	241	7 ADG25980	ADG25980 Human pro
28	453	80.3	241	7 ADN39286	ADN39286 Cancer/an
29	453	80.3	258	5 ABG96433	ABG96433 Human ova
30	453	80.3	258	7 ADB75599	ADB75599 Prostate
31	453	80.3	273	2 AAW61618	AAW61618 Clone HPW
32	453	80.3	273	7 ABW01500	ABW01500 Human rec
33	453	80.3	273	9 ABB98431	ABB98431 Human HPW
34	436.5	77.4	240	5 ABB89113	ABB89113 Human pol
35	401	71.1	121	5 ABP43214	ABP43214 Human ova
36	396	70.2	156	8 ADT50975	ADT50975 Cancer re
37	396	70.2	156	8 ADT50970	ADT50970 Cancer re
38	365	64.7	103	5 ABP32558	ABP32558 Human gly
39	358	63.5	126	2 AAY35991	AAY35991 Extended
40	358	63.5	126	8 ADP19299	ADP19299 Human sec
41	357.5	63.4	241	5 ABB09512	ABB09512 Human TSP
42	357.5	63.4	241	8 ADO10063	ADO10063 Novel hum
43	353.5	62.7	207	8 ADT50972	ADT50972 Cancer re
44	316	56.0	101	2 AAY13159	AAY13159 Human sec
45	315	55.9	108	2 AAY11883	AAY11883 Human 5'

ALIGNMENTS

RESULT 1

AAW47275
ID AAW47275 standard; protein; 99 AA.

XX AAW47275;
XX
XX 02-JUL-1998 (first entry)
XX
XX Human HPK-1A C4.8 protein.
XX
XX Cervical cancer; treatment; diagnosis; passage cell; lesion;
KW human foreskin keratinocyte cell line; HPK-1A; antibody; smear.
XX
XX Homo sapiens.
XX
XX DE19649207-C1.
XX
XX 26-FEB-1998.
XX
XX 27-NOV-1996; 96DE-01049207.
XX
XX 27-NOV-1996; 96DE-01049207.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Duerst M, Nees M;
XX WPI; 1998-121623/12.
XX N-PSDB; AAV15588.
XX Nucleic acid characteristic of late or early passage cells immortalised
PT by papilloma virus - and related polypeptide(s) and antibodies, used for
PT diagnosis and treatment of cervical cancer and assessing potential for

PT progression of cervical lesions.
 XX Claim 2; Fig 1; 8pp; German.
 XX This protein, C4.8, is derived from a human papillomavirus (HPV)
 CC immortalised human foreskin keratinocyte cell line HPK-1A and is
 CC characteristic of late or early passage cells. This sequence is used in a
 CC method for assessing the potential for progression of cervical lesions.
 CC Antibodies generated against the encoded polypeptide are used for
 CC diagnosis of cervical cancer and to assess potential for lesion
 CC progression. Antibodies can also be used therapeutically by inhibiting
 CC the polypeptide. Antisense molecules based on the nucleotide sequence are
 CC used to inhibit expression of the protein. Detecting polypeptides, or
 CC related RNA, characteristic of late passage cells (which are potentially
 CC malignant) in cervical smears is a reliable way of assessing progression
 CC potential
 XX Sequence 99 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2.24e-49 Length: 99
 Score: 484.00 Matches: 99
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 85.8% Indels: 0
 DB: 2 Gaps: 0
 US-10-079-954-1 (1-297) x AAM47275 (1-99)
 QY 1 GCAATCGATGGGCATCTCTTCTGAAGATCTTCGGGCACATGCTCGTCAGTGCATGCAG 60
 DB 1 AlallepGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 20
 QY 61 TTTGTCAACGTGGGCTACTTCTCATCGACCGCGGTGTGGTCTTGTCTTGGTTTC 120
 DB 21 PheValAenValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 40
 QY 121 CTGGGCTGCTATGCTTAACTGAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 41 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 60
 QY 181 CTCTCTCTCATCTTCATCTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 61 LeuLeuLeuIlePheIleAlaGluValAlaAlaAlaValAlaLeuValTyrIle 80
 QY 241 ATGGCTGAGCACTTCCCGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
 DB 81 MetAlaGluHisPheProThrLeuLeuValValProAlaIleLysLysIleMetVal 99
 RESULT 2
 ID ADR65994 standard; protein; 214 AA.
 XX
 AC ADR65994;
 XX
 XX
 DT 02-DEC-2004 (first entry)
 XX
 XX Human prostatic carcinoma derived protein SEQ ID 190 #1.
 XX human; cytostatic; diagnosis; prostatic cancer;
 KW differential expression analysis.
 XX
 OS Homo sapiens.
 XX
 FN WO2004076614-A2.
 XX
 PD 10-SEP-2004.
 XX
 XX 22-FEB-2004; 2004WO-DE000433.
 XX
 XX 27-FEB-2003; 2003DE-01009985.
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 XX
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 XX
 PI Hinzmann B, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
 PI Xinzhang L, Staub E;
 XX
 DR WPI; 2004-653386/63.
 XX
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 PT agents.
 XX
 PS Claim 2; Page 585; 1607pp; German.
 XX
 CC This invention describes novel cytostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.
 XX
 SQ Sequence 214 AA;
 Alignment Scores:
 Pred. No.: 1.52e-45 Length: 214
 Score: 453.00 Matches: 93
 Percent Similarity: 97.9% Conservative: 1
 Best Local Similarity: 96.9% Mismatches: 2
 Query Match: 80.3% Indels: 0
 DB: 8 Gaps: 0
 US-10-079-954-1 (1-297) x ADR65994 (1-214)
 QY 1 GCAATCGATGGGCATCTCTTCTGAAGATCTTCGGGCACATGCTCGTCAGTGCATGCAG 60
 DB 6 SerileaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 25
 QY 61 TTTGTCAACGTGGGCTACTTCTCATCGACCGCGGTGTGGTCTTGTCTTGGTTTC 120
 DB 26 PheValAenValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 45
 QY 121 CTGGGCTGCTATGCTTAACTGAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 46 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 65

Db 64 LeuGlyCysrYrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheIle 83
 Qy 181 CTCCTCCTCATCTTCATCTGAGGTTGCAGCTGCTGGTGGCTGGTGTACACCAT 240
 Db 84 LeuLeuLeuPhePheIleAlaGluValAlaAlaValAlaLeuValTyrThr 103
 Qy 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAAG 288
 Db 104 MetAlaGluHisPheLeuThrLeuLeuValProAlaIleLysLys 119

RESULT 5
 ABO1936
 ID ABO01936 standard; protein; 233 AA.
 AC ABO01936;
 XX
 DT 12-AUG-2003 (first entry)
 XX
 DE Novel human secreted protein #4.
 XX
 KW Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
 KW immune system disorder; haematopoietic cell disorder;
 KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
 KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
 KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;
 KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
 KW glomerulonephritis; Grave's disease; allergic reaction;
 KW graft-versus-host disease; hyperproliferative disorder; neoplasm;
 KW infectious disease; nervous system disease; spinal cord disorder;
 KW head trauma; stroke; tissue regeneration; congenital defect; trauma;
 KW wound; burn; incision; ulcer; age disease; osteoporosis;
 KW periodontal disease; liver failure; catabolism; anabolism; metabolism;
 KW food additive; preservative; secreted protein.
 XX
 OS Homo sapiens.
 XX
 FN US2003027132-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 04-SEP-1998; 98US-00148545.
 XX
 PR 07-MAR-1997; 97US-0038621P.
 PR 07-MAR-1997; 97US-0040161P.
 PR 07-MAR-1997; 97US-0040162P.
 PR 07-MAR-1997; 97US-0040163P.
 PR 07-MAR-1997; 97US-0040333P.
 PR 07-MAR-1997; 97US-0040334P.
 PR 07-MAR-1997; 97US-0040336P.
 PR 07-MAR-1997; 97US-0040626P.
 PR 11-APR-1997; 97US-0043311P.
 PR 11-APR-1997; 97US-0043312P.
 PR 11-APR-1997; 97US-0043313P.
 PR 11-APR-1997; 97US-0043314P.
 PR 11-APR-1997; 97US-0043315P.
 PR 11-APR-1997; 97US-0043568P.
 PR 11-APR-1997; 97US-0043569P.
 PR 11-APR-1997; 97US-0043576P.
 PR 11-APR-1997; 97US-0043578P.
 PR 11-APR-1997; 97US-0043580P.
 PR 11-APR-1997; 97US-0043669P.
 PR 11-APR-1997; 97US-0043670P.
 PR 11-APR-1997; 97US-0043671P.
 PR 11-APR-1997; 97US-0043672P.
 PR 23-MAY-1997; 97US-0043674P.
 PR 23-MAY-1997; 97US-0047492P.
 PR 23-MAY-1997; 97US-0047500P.
 PR 23-MAY-1997; 97US-0047501P.
 PR 23-MAY-1997; 97US-0047502P.
 PR 23-MAY-1997; 97US-0047503P.
 PR 23-MAY-1997; 97US-0047581P.
 PR 23-MAY-1997; 97US-0047582P.
 PR 23-MAY-1997; 97US-0047583P.
 PR 23-MAY-1997; 97US-0047584P.
 PR 23-MAY-1997; 97US-0047585P.
 PR 23-MAY-1997; 97US-0047586P.
 PR 23-MAY-1997; 97US-0047587P.
 PR 23-MAY-1997; 97US-0047588P.
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 PR 23-MAY-1997; 97US-0047590P.
 PR 23-MAY-1997; 97US-0047592P.
 PR 23-MAY-1997; 97US-0047593P.
 PR 23-MAY-1997; 97US-0047594P.
 PR 23-MAY-1997; 97US-0047595P.
 PR 23-MAY-1997; 97US-0047596P.
 PR 23-MAY-1997; 97US-0047597P.
 PR 23-MAY-1997; 97US-0047598P.
 PR 23-MAY-1997; 97US-0047599P.
 PR 23-MAY-1997; 97US-0047600P.
 PR 23-MAY-1997; 97US-0047601P.
 PR 23-MAY-1997; 97US-0047612P.
 PR 23-MAY-1997; 97US-0047613P.
 PR 23-MAY-1997; 97US-0047614P.
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 PR 23-MAY-1997; 97US-0047617P.
 PR 23-MAY-1997; 97US-0047618P.
 PR 23-MAY-1997; 97US-0047632P.
 PR 06-JUN-1997; 97US-0048964P.
 PR 06-JUN-1997; 97US-0048974P.
 PR 22-AUG-1997; 97US-0056630P.
 PR 22-AUG-1997; 97US-0056631P.
 PR 22-AUG-1997; 97US-0056632P.
 PR 22-AUG-1997; 97US-0056636P.
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 PR 22-AUG-1997; 97US-0056664P.
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 PR 22-AUG-1997; 97US-0056878P.
 PR 22-AUG-1997; 97US-0056879P.
 PR 22-AUG-1997; 97US-0056880P.
 PR 22-AUG-1997; 97US-0056881P.
 PR 22-AUG-1997; 97US-0056882P.
 PR 22-AUG-1997; 97US-0056884P.
 PR 22-AUG-1997; 97US-0056886P.
 PR 22-AUG-1997; 97US-0056887P.
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 PR 22-AUG-1997; 97US-0056908P.
 PR 22-AUG-1997; 97US-0056909P.
 PR 22-AUG-1997; 97US-0056910P.
 PR 22-AUG-1997; 97US-0056911P.
 PR 05-SEP-1997; 97US-0057650P.
 PR 05-SEP-1997; 97US-0057761P.
 PR 06-MAR-1998; 98WO-US004482.
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (FISC/) FISCHER C L.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D R.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.


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PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043673P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047452P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
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PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
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PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047616P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
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PR 22-AUG-1997; 97US-0056872P.
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PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.

PR 06-MAR-1998; 98WO-US004482.
PR 04-SEP-1998; 98US-00148545.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Rosen CA, Komatsoulis G, Shi Y;
XX WPI; 2005-293232/30.
XX N-PSDB; ADZ12214.
XX New human secreted protein that activates the interferon-sensitive
XX responsive promoter element, useful for diagnosing and treating
XX cerebellum disorders, rheumatoid arthritis, sepsis, ischemia and cancer.
XX Example 1; SEQ ID NO 137; 230pp; English.
XX The invention relates to an isolated human secreted protein comprising
XX amino acid residues 23-230, 2-230 or 1-230 of the 231 amino acid sequence
XX of ADZ12415, where the isolated protein has the function of activating
XX the interferon-sensitive responsive promoter element. Also described: (1)
XX a composition comprising the protein and a pharmaceutical carrier; and
XX (2) producing the isolated protein by expressing the protein in a cell,
XX and recovering the protein. The protein is useful in reagents for the
XX differential identification of tissue(s) or cell type(s) present in a
XX biological sample. It can also be used for diagnosing and treating
XX diseases and conditions such as cerebellum disorders, rheumatoid
XX arthritis, sepsis, ischemia, thrombosis, cancer, infertility, impotence,
XX cardiovascular and neurological disorders. The protein can also be useful
XX for producing immunological probes. The present sequence represents a
XX human secreted protein from the present invention.
XX SQ Sequence 233 AA;

Alignment Scores:
Pred. No.: 1,55e-45 Length: 233
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 9 Gaps: 0

US-10-079-954-1 (1-297) x ADZ12337 (1-233)
QY 1 GCAATCGATGGGCACTCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAG 60
DB ::::|||||AlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 43
QY 61 TTTGTCAAGCTGGGCTACTTCTTCATCGCAGCCGGCTGTGTGCTTTGCTCTTGGTTTC 120
DB |||||PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 63
QY 121 CTGGGCTGCTAGTCTAAGACTGAGACGAGTGTGCGCTGCTGCTGGTGTACACATA 240
DB |||||LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThr 103
QY 241 ATGGCTGAGCACTTCCGACGCTGTGGTAGTGCCTGCCATCAAGAAG 288
DB |||||MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 119

RESULT 7
AAG62153
ID AAG62153 standard; protein; 240 AA.
XX AAG62153;
XX AC
XX XX
XX DT 06-JUL-2001 (first entry)
XX XX
XX DE Human P503S inventive antigen SEQ ID NO: 352.
XX XX

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RESULT 9
AAW59954
ID AAW59954 standard; protein; 241 AA.
XX AC AAW59954;
XX DT 02-DEC-1998 (first entry)
XX DE Amino acid sequence of the human tumour-associated antigen.
XX DE Human; tumour-associated antigen; PRAT; stimulation; cell proliferation;
XX KW antagonist; cancer; genetic defect; sickle cell anaemia; agonist;
XX KW antibody; hybridisation; probe.
XX XX
XX OS Homo sapiens.
XX PN WO9838310-A1.
XX PD 03-SEP-1998.
XX PF 27-FEB-1998; 98WO-US003953.
XX PR 28-FEB-1997; 97US-00808148.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Hillman JL, Goli SK;
XX DR WPI; 1998-481208/41.
XX DR N-PSDB; AAW54014.
XX PT Human tumour-associated antigen PRAT - useful for stimulating cell
XX proliferation and screening for antagonists useful to treat or prevent
XX cell proliferation disorders e.g. cancers.
XX PS Disclosure; Fig 1A-1C; 5app; English.
XX
XX CC This is the amino acid sequence of the human tumour-associated antigen
XX (PRAT) used in the method of the invention for stimulating cell
XX proliferation and screening for antagonists useful to treat or prevent
XX cell proliferation disorders such as cancer, and genetic defect e.g.
XX sickle cell anaemia. The polypeptides can be combined with a suitable
XX carrier in pharmaceutical compositions, and also used to screen for
XX antagonists, agonists, and to generate antibodies. PRAT agonists can be
XX added to a cell to stimulate cell proliferation by increasing or
XX prolonging the activity of PRAT as above. The antagonists can be combined
XX with a suitable carrier in pharmaceutical compositions, which can be
XX administered to subjects to treat or prevent disorders associated with
XX cell proliferation, especially cancers. Antibodies specific for PRAT may
XX be used directly as antagonists, or indirectly as a targeting or delivery
XX mechanism to bring pharmaceutical agents to PRAT-expressing cells. They
XX are also useful to diagnose conditions or diseases characterised by PRAT
XX expression and to monitor therapeutic interventions. The polynucleotide
XX encoding PRAT, or complementary sequences, can be used to produce
XX hybridisation probes, useful to detect polynucleotides or fragments
XX encoding PRAT, e.g. to diagnose diseases relating to polypeptide
XX expression or monitor PRAT regulation during therapeutic intervention
XX
XX SQ Sequence 241 AA;
Alignment Scores:
Pred. No.: 1,56e-45 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 2 Gaps: 0
US-10-079-954-1 (1-297) x AAW59954 (1-241)
QY 1 GCATCGATGGGCGATCTTCTGAAGATCTTCGGGCGACATGTCTCGTCAGTCCATGCGAG 60
DB 33 SerileAspGlyValaSerPheLeuIlylePheGlyProLeuSerSerAlaMetGln 52

Db 33 SerlleaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
 Qy 61 TTTGTCAAGTGGGCTACTTCTCATCGACCGCGGTGGTCTTTGGCTTCTGGTTTC 120
 Db 53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValValPheAlaLeuGlyPhe 72
 Qy 121 CTGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
 Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
 Qy 181 CTCTCTCTCATCTTCCAGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACCATTA 240
 Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValValThrThr 112
 Qy 241 ATGGCTGAGCACTTCCGACGCTTGTGCTGTAGTGTGCTGCCATCAAGAAG 288
 Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 11
 AAW58380
 ID AAW58380 standard; protein; 241 AA.
 XX
 AC AAW58380;
 DT 14-SEP-1998 (first entry)
 XX
 DE Human secreted protein AR415_4.
 XX
 KW AR415_4; secreted protein; protein factor; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 14..26
 FT /note= "putative leader/signal peptide or transmembrane
 FT domain"
 FT Protein 27..241
 FT /label= Mat_protein
 XX
 WO9817687-A2.
 XX
 PD 30-APR-1998.
 XX
 PF 24-OCT-1997; 97WO-US019590.
 XX
 PR 25-OCT-1996; 96US-00740274.
 PR 24-OCT-1997; 97US-00740274.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX
 DR WPI; 1998-261426/23.
 DR N-PSDB; AAV30916.
 XX
 PT Nucleic acid encoding secreted protein from human cells - useful, e.g. as
 PT immuno-modulators, anti-tumour agents, promoters of tissue growth,
 PT haemostatic and thrombolytic agents etc.
 XX
 PS Claim 8; Page 67-68; 114pp; English.
 XX
 CC This polypeptide, designated AT415_4, is a novel human secreted protein.
 CC Its amino acid sequence was deduced from a full-length AT415_4 cDNA clone
 CC (see AAV30916) isolated from a human adult retina cDNA library. The
 CC predicted amino acid sequence shows homology to human AAM35252 and CO-029
 CC tumour associated antigens, and computer predictions suggest a potential
 CC transmembrane domain centered around amino acid 100 of the protein. 11
 CC Novel human secreted proteins (see AAW58380-90) are claimed. These can be
 CC expressed in recombinant host cells for analysis, characterisation,
 CC diagnostic or therapeutic use. They can also be used as tissue or mol.wt.
 CC markers, to generate antibodies, and in interaction trap assays. They may
 CC have biological activities, e.g. cytokine, immunomodulator,

CC haematopoiesis regulating activity, tissue growth activity, activin or
 CC inhibin activity, chemotactic or chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, antiinflammatory.
 CC cadherin and tumour invasion suppressor activity, and tumour inhibition
 CC activity. The proteins can be expressed in vivo from DNA, introduced in
 CC gene therapy vectors
 XX
 SQ Sequence 241 AA;
 Alignment Scores: 1.56e-45 Length: 241
 Pred. No.: 453.00 Matches: 93
 Score: 97.9% Conservative: 1
 Percent Similarity: 96.9% Mismatches: 2
 Best Local Similarity: 80.3% Indels: 0
 Query Match: 2 Gaps: 0
 DB: 2
 US-10-079-954-1 (1-297) x AAW58380 (1-241)
 Qy 1 GCATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATCGAG 60
 Db 33 SerlleaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
 Qy 61 TTTGTCAAGTGGGCTACTTCTCATCGACCGCGGTGGTCTTTGGCTTCTGGTTTC 120
 Db 53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
 Qy 121 CTGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
 Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
 Qy 181 CTCTCTCTCATCTTCCAGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACCATTA 240
 Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValValThrThr 112
 Qy 241 ATGGCTGAGCACTTCCGACGCTTGTGCTGTAGTGTGCTGCCATCAAGAAG 288
 Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 12
 AAY82003
 ID AAY82003 standard; protein; 241 AA.
 XX
 AC AAY82003;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human immunogenic prostate tumour protein sequence SEQ ID NO:114.
 XX
 KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
 KW immunogenic; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200004149-A2.
 XX
 PD 27-JAN-2000.
 XX
 PF 14-JUL-1999; 99WO-US015838.
 XX
 PR 14-JUL-1998; 98US-00115453.
 PR 14-JUL-1998; 98US-00116134.
 PR 23-SEP-1998; 98US-00159812.
 PR 23-SEP-1998; 98US-00159822.
 PR 15-JAN-1999; 99US-00232149.
 PR 15-JAN-1999; 99US-00232880.
 PR 09-APR-1999; 99US-00288946.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
 XX
 DR WPI; 2000-171268/15.

XX 19-JUL-2001.
PD 16-JAN-2001; 2001WO-US001574.
XX 14-JAN-2000; 2000US-00483672.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX WPI; 2001-425973/45.
DR New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
PT Claim 2; Page 268-269; 543pp; English.
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I). (II).
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AA01115 to AA01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX SQ Sequence 241 AA;
Alignment Scores:
Pred. No.: 1.56e-45 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 4 Gaps: 0
US-10-079-954-1 (1-297) x AA01118 (1-241)
QY 1 GCAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCATGCAG 60
DB 33 SerileAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
QY 61 TTGTGCAACGTGGGCTACTTCTCATCGCAGCCGGCGTGTGGTCTTTGCTCTTGGTTTC 120
DB 53 PheValAsnValGlyTyPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGCTGCTATGTCCTAAGACTGAGAGAGAGTGCCTCGTGCATCTTCTTCTATC 180
DB 73 LeuGlyCySerTyGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheile 92
QY 181 CTCCTCCATCTTCATGCTGAGGTTCGAGCTGCTGTGTGGTGTGGTGTACACCATTA 240
DB 93 LeuLeuLeuIlePheileAlaGluValAlaAlaAlaValAlaValValTyrrThr 112
QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCGCATCAAGAAG 288
DB 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128
RESULT 15
AAU69764
ID AAU69764 standard; protein; 241 AA.
XX AC AAU69764;

XX 30-JAN-2002 (first entry)
DT Human prostate cDNA encoded protein #4.
XX Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
XX Homo sapiens.
XX WO200173032-A2.
XX 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US009919.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.
DR N-PSDB; AAS63558.
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX Claim 2; Page 270-271; 579pp; English.
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polypeptide of the invention
XX SQ Sequence 241 AA;
Alignment Scores:
Pred. No.: 1.56e-45 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 4 Gaps: 0
US-10-079-954-1 (1-297) x AAU69764 (1-241)
QY 1 GCAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCATGCAG 60
DB 33 SerileAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
QY 61 TTGTGCAACGTGGGCTACTTCTCATCGCAGCCGGCGTGTGGTCTTTGCTCTTGGTTTC 120
DB 53 PheValAsnValGlyTyPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72

Qy	121	CTGGCTGCTATGGTGTCTAAGACTGAGACGAGCAAGTGTGCCCTCGTACGTTCTTCTTCATC	180
Db	73	LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheIle	92
Qy	181	CTCCTCCTCATCTTCATTGCTGAGTTGCGAGTTCGAGCTGTGTGGTGGTGTGTACACCATATA	240
Db	93	LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValThrThr	112
Qy	241	ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAG	288
Db	113	MetAlaGluHisPheLeuThrLeuLeuValProAlaIleLysLys	128

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Job time : 114.645 secs

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 12:06:50 ; Search time 129 Seconds
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Title: US-10-079-954-1

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- 6: /cgn2_6/ptodata/1/ina/PCFUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	3	US-09-308-984-1
2	282.8	95.2	933	3	US-08-808-148-2
3	282.8	95.2	1289	3	US-09-020-956-111
4	282.8	95.2	1289	3	US-09-030-607-111
5	282.8	95.2	1289	3	US-09-439-313-111
6	282.8	95.2	1289	3	US-09-352-616A-111
7	282.8	95.2	1289	3	US-09-232-149A-111
8	282.8	95.2	1289	3	US-09-159-812-111
9	282.8	95.2	1289	3	US-09-636-215-111
10	282.8	95.2	1289	3	US-09-685-166A-111
11	282.8	95.2	1289	3	US-09-115-453-111
12	282.8	95.2	1289	3	US-09-688-489-111
13	282.8	95.2	1289	3	US-09-679-426-111
14	282.8	95.2	1289	3	US-09-759-143-111
15	282.8	95.2	1289	3	US-09-651-236-111
16	282.8	95.2	1289	3	US-09-030-606-111
17	282.8	95.2	1289	3	US-09-657-279-111
18	282.8	95.2	1289	3	US-10-012-896-82
19	282.8	95.2	1324	3	US-09-148-545-11
20	282.8	95.2	1324	3	US-09-621-011-82
21	282.8	95.2	1376	3	US-09-148-545-14
22	282.8	95.2	1376	3	US-09-621-011-14
23	282.8	95.2	1533	3	US-09-807-201-14
24	272.8	91.9	740	3	US-09-020-956-17

ALIGNMENTS

RESULT 1

US-09-308-984-1
; Sequence 1, Application US/09308984
; Patent No. 6388065
; GENERAL INFORMATION:
; APPLICANT: Durst, Matthias
; APPLICANT: Nees, Matthias
; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
; FILE REFERENCE: SCHU 204 (09902857)
; CURRENT APPLICATION NUMBER: US/09/308,984
; PRIOR APPLICATION NUMBER: PCT/DE97/02660
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: DE 196 49207
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-308-984-1

Query Match 100.0%; Score 297; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.1e-78;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCATCGATGGGCATCCTTCTGAAGATCTTCGGGCCACTGCTCCAGTGCATGCAG 60	
Db	1	GCATCGATGGGCATCCTTCTGAAGATCTTCGGGCCACTGCTCCAGTGCATGCAG 60	
Qy	61	TTTGTCAAAGTGGGCTACTTCTCATCGACGCGGTTGTTGCTTTTGTCTTTGGTTTC 120	
Db	61	TTTGTCAAAGTGGGCTACTTCTCATCGACGCGGTTGTTGCTTTTGTCTTTGGTTTC 120	
Qy	121	CTGGGCTGCTATGGTCTAAGACTGAGACAGTGTGCCCTCGTACGTTTCTTTCATC 180	
Db	121	CTGGGCTGCTATGGTCTAAGACTGAGACAGTGTGCCCTCGTACGTTTCTTTCATC 180	
Qy	181	CTCCTCTCATCTTCTTCTGAGGTTGAGCTGCTGTGCTGCTGCTGCTGCTGCTGCT 240	
Db	181	CTCCTCTCATCTTCTTCTGAGGTTGAGCTGCTGTGCTGCTGCTGCTGCTGCTGCT 240	
Qy	241	ATGGCTGAGCAGCTTCCCGAGGTTGCTGGTAGTGCCTGCCATCAAGAAGATTATGGTT 297	
Db	241	ATGGCTGAGCAGCTTCCCGAGGTTGCTGGTAGTGCCTGCCATCAAGAAGATTATGGTT 297	

APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 61
Db 220 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 279
Qy 62 TTGTCACAGTGGGCTACTTCTCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTC 121
Db 280 TTGTCACAGTGGGCTACTTCTCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTC 339
Qy 122 TGGGCTGCTATGGTGCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 181
Db 340 TGGGCTGCTATGGTGCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 399
Qy 182 TCCTCTCATCTTCATTGCTGAGGTTCGAGCTGCTGTGGTGCCTTGGTGACACCAATAA 241
Db 400 TCCTCTCATCTTCATTGCTGAGGTTCGAGCTGCTGTGGTGCCTTGGTGACACCAATAA 459
Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCTGCTGCATCAAGAA 287
Db 460 TGGCTGAGCACTTCTCTGACGTTGCTGTAGTGCTGCTGCATCAAGAA 505

RESULT 5
US-09-439-313-111
; Sequence 111, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi

APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 111
LENGTH: 1289
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 61
Db 220 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 279
Qy 62 TTGTCACAGTGGGCTACTTCTCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTC 121
Db 280 TTGTCACAGTGGGCTACTTCTCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTC 339
Qy 122 TGGGCTGCTATGGTGCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 181
Db 340 TGGGCTGCTATGGTGCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 399
Qy 182 TCCTCTCATCTTCATTGCTGAGGTTCGAGCTGCTGTGGTGCCTTGGTGACACCAATAA 241
Db 400 TCCTCTCATCTTCATTGCTGAGGTTCGAGCTGCTGTGGTGCCTTGGTGACACCAATAA 459
Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCTGCTGCATCAAGAA 287
Db 460 TGGCTGAGCACTTCTCTGACGTTGCTGTAGTGCTGCTGCATCAAGAA 505

RESULT 6
US-09-352-616A-111
; Sequence 111, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 111
LENGTH: 1289
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 61
Db 220 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 279

Db 460 TGGCTGAGCACTTCCTGACGTTGCTGTAGTGTGCTGCTGCCATCAAGAA 505

RESULT 15

US-09-651-236-111
; Sequence 111, Application US/09651236
; Patent No. 6818751

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 111

; LENGTH: 1289

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-651-236-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCCATGCAGT	61
Db	220	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCCATGCAGT	279
Qy	62	TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTTGTGGTCTTTGCTCTTGGTTTCC	121
Db	280	TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTTGTGGTCTTTGCTCTTGGTTTCC	339
Qy	122	TGGGCTGTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	181
Db	340	TGGGCTGTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	399
Qy	182	TCCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGGCCCTTGGTGACCAATAA	241
Db	400	TCCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGGCCCTTGGTGACCAATAA	459
Qy	242	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA	287
Db	460	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA	505

Search completed: March 23, 2006, 12:10:19
Job time : 130 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 11:01:04 ; Search time 475 Seconds
(without alignments)
4167.187 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 297

Sequence: 1 gcaatcgatgggcacccctt.....ccatcaagaagattatggtt 297

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	2	AAV15588 Human HPK
2	282.8	95.2	513	5	AAF93382 Lung carc
3	282.8	95.2	624	14	ACL62169 Human col
C 4	282.8	95.2	635	4	AAI29471 Colon tum
C 5	282.8	95.2	635	8	ABZ33657 Human col
6	282.8	95.2	792	6	ABK29835 Colon ade
7	282.8	95.2	933	2	AAV54014 Nucleotid
8	282.8	95.2	1044	14	ABE35193 Human Gef
9	282.8	95.2	1076	6	ABE76533 cDNA enco
10	282.8	95.2	1076	10	ADB75600 Prostate
11	282.8	95.2	1076	13	ADR25330 Breast ca
12	282.8	95.2	1076	13	ADR65868 Human pro
13	282.8	95.2	1076	13	ADR66771 Human pro
14	282.8	95.2	1077	13	ADQ85081 Human tum
15	282.8	95.2	1154	6	ABE76532 cDNA enco
16	282.8	95.2	1154	10	ADB75598 Prostate
17	282.8	95.2	1278	11	ADN39285 Cancer/an
18	282.8	95.2	1288	2	AAV48113 Nucleotid
C 19	282.8	95.2	1288	10	AAD62626 DNA #4 us

20	282.8	95.2	1288	10	AAD62609	Aad62609 Human rec
21	282.8	95.2	1289	2	AAV58587	Aav58587 prostate
22	282.8	95.2	1289	2	AAV61202	Aav61202 Full leng
23	282.8	95.2	1289	3	ABE71255	AbE71255 Human pro
24	282.8	95.2	1289	4	AAH93466	Aah93466 Human pro
25	282.8	95.2	1289	4	AAAG3558	Aag63558 Human pro
26	282.8	95.2	1289	4	AAH02531	Aah02531 Prostate
27	282.8	95.2	1289	4	AAH84780	Aah84780 Human pro
28	282.8	95.2	1289	4	AAF86954	Aaf86954 Human P50
29	282.8	95.2	1289	5	ACA59367	Aca59367 Prostate
30	282.8	95.2	1289	5	AAS10109	Aas10109 Human pro
31	282.8	95.2	1289	6	ABL94930	Adl94930 Human N1-
32	282.8	95.2	1289	6	ABE58639	ABe58639 Prostate
33	282.8	95.2	1289	8	ACC95094	Acc95094 Prostate
34	282.8	95.2	1289	10	ADB13561	Adb13561 Human pro
35	282.8	95.2	1289	10	ADG25977	Adg25977 Human pro
36	282.8	95.2	1290	3	AAA06350	Aaa06350 Human imm
37	282.8	95.2	1306	13	ADR44012	Adr44012 Human bre
38	282.8	95.2	1324	2	AAV34225	Aav34225 Human sec
39	282.8	95.2	1324	8	ACD08096	AcD08096 cDNA enco
40	282.8	95.2	1324	14	AD212282	Ad212282 Human sec
41	282.8	95.2	1376	2	AAV34157	Aav34157 Human sec
42	282.8	95.2	1376	8	ACD08028	AcD08028 cDNA enco
43	282.8	95.2	1376	14	AD212214	Ad212214 Human sec
44	282.8	95.2	1456	9	ADA11015	Ada11015 Human cDN
45	282.8	95.2	1533	3	AAZ95011	Aaz95011 Cancer sp

ALIGNMENTS

RESULT 1

AAV15588

ID AAV15588 standard; DNA; 297 BP.

XX AC AAV15588;

DT 02-JUL-1998 (first entry)

XX Human HPK-1A C4.8 DNA.

DE Cervical cancer; treatment; diagnosis; passage cell; lesion;

XX human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.

OS Homo sapiens.

XX DE19649207-Cl.

FN 26-FEB-1998.

XX 27-NOV-1996; 96DE-01049207.

XX 27-NOV-1996; 96DE-01049207.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Duerst M, Nees M;

XX WPI; 1998-121623/12.

XX P-PSDB; AAW47275.

XX Nucleic acid characteristic of late or early passage cells immortalised

XX by papilloma virus - and related polypeptide(s) and antibodies, used for

XX diagnosis and treatment of cervical cancer and assessing potential for

XX progression of cervical lesions.

XX Claim 2; Fig 1; 8pp; German.

XX This sequence, C4.8, is derived from a human papillomavirus (HPV)

XX immortalised human foreskin keratinocyte cell line HPK-1A and is

XX characteristic of late or early passage cells. This sequence is used in a

XX method for assessing the potential for progression of cervical lesions.

XX Antibodies generated against the encoded polypeptide are used for

CC diagnosis of cervical cancer and to assess potential for lesion
CC progression. Antibodies can also be used therapeutically by inhibiting
CC the polypeptide. Antisense molecules based on the nucleotide sequence are
CC used to inhibit expression of the protein. Detecting polypeptides, or
CC related RNA, characteristic of late passage cells (which are potentially
CC malignant) in cervical smears is a reliable way of assessing progression
CC potential
XX
SQ Sequence 297 BP; 46 A; 79 C; 80 G; 92 T; 0 U; 0 Other;
Query Match 100.0%; Score 297; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAG 60
Db 1 GCAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAG 60
Qy 61 TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCTTGCTTGGCTTGGTTTC 120
Db 61 TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCTTGCTTGGCTTGGTTTC 120
Qy 121 CTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
Db 121 CTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
Qy 181 CTCTCCCTCATCTTCATTCGTGAGGTTGCAGCTGCTGTGTCGGCTTGGTGTACACCAT 240
Db 181 CTCTCCCTCATCTTCATTCGTGAGGTTGCAGCTGCTGTGTCGGCTTGGTGTACACCAT 240
Qy 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCGCATCAAGAGATTATGGTT 297
Db 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCGCATCAAGAGATTATGGTT 297
RESULT 2
AAF93382
ID AAF93382 standard; cDNA; 513 BP.
AC AAF93382;
XX
XX 21-MAY-2001 (first entry)
XX
DE Lung carcinoma cDNA encoding SRT protein SEQ ID 203.
XX
XX Human; SRT; gene therapy; gene mapping; tissue typing; ss.
XX
XX Homo sapiens.
XX
XX WO200107611-A2.
XX
XX 01-FEB-2001.
XX
XX 21-JUL-2000; 2000WO-US020006.
XX
XX 26-JUL-1999; 99US-0145701P.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Goddard A, Wood WI;
XX
XX WPI; 2001-112729/12.
XX
XX New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT for production of recombinant SRT polypeptides, gene mapping, diagnosing
PT genetic disorders and for gene therapy.
XX
XX
PS Claim 2; Fig 203; 663pp; English.
XX
CC Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC human SRT proteins. The cDNA sequences are isolated from various
CC different human tissue cDNA libraries. The invention relates to a method
CC for detecting cDNA encoding an SRT protein, a vector containing cDNA

CC encoding SRT, a host cell transformed with the vector, an isolated SRT
CC polypeptide, and an antibody which binds to SRT. The polynucleotide
CC sequence can be used in gene therapy and is useful in the recombinant
CC production of SRT polypeptides, as a hybridisation probe to screen
CC libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC map the gene encoding the SRT polypeptides and analysing genetic
CC disorders, tissue typing and disease tissue detection. The SRT
CC polynucleotide sequences can be used in polymerase chain reaction,
CC screening for new therapeutic molecules and generation of antisense RNA
CC and DNA
XX
SQ Sequence 513 BP; 97 A; 135 C; 129 G; 152 T; 0 U; 0 Other;
Query Match 95.2%; Score 282.8; DB 5; Length 513;
Best Local Similarity 99.3%; Pred. No. 8.1e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAGT 61
Db 99 CAATCGATGGGGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAGT 158
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCTTGCTTGGCTTGGTTTC 121
Db 159 TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCTTGCTTGGCTTGGTTTC 218
Qy 122 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 219 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 278
Qy 182 TCCTCCCTCATCTTCATTCGTGAGGTTGCAGCTGCTGTGTCGGCTTGGTGTACACCAT 241
Db 279 TCCTCCCTCATCTTCATTCGTGAGGTTGCAGCTGCTGTGTCGGCTTGGTGTACACCA 338
Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCGCATCAAGAA 287
Db 339 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCGCATCAAGAA 384
RESULT 3
ACL62169
ID ACL62169 standard; cDNA; 624 BP.
AC ACL62169;
XX
XX 24-MAR-2005 (first entry)
DT
XX
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:8304.
XX
XX Differential expression; diagnosis; therapy; drug screening; cancer;
XX neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200500087-A2.
XX
XX 06-JAN-2005.
XX
XX 13-MAY-2004; 2004WO-US015421.
XX
XX 03-JUN-2003; 2003US-0475872P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Randazzo F, Moler E, Escobedo J, Garcia PD;
XX
XX WPI; 2005-075421/08.
XX
XX New isolated polynucleotides, which are differentially expressed in colon
PT cancer cell, useful for treating cancer, e.g. colon cancer, breast
PT cancer, or pancreatic cancer.
XX
XX Claim 1; SEQ ID NO 8304; 97pp; English.

XX The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which
 CC are differentially expressed in colon cancer cells. The invention also
 CC relates to vectors and host cells comprising a differentially expressed
 CC polynucleotide of the invention; a method for detecting a cancerous cell
 CC by detection of a gene product of the polynucleotides; a method for
 CC inhibiting a cancerous phenotype of a cell by inhibiting a gene product
 CC of the polynucleotides; a method of treating an individual with cancer by
 CC administration of a modulator of a gene product of the polynucleotides;
 CC and an isolated antibody that specifically binds to a polypeptide encoded
 CC by one of the 9672 polynucleotides. The polynucleotides, polypeptides,
 CC antibodies, and methods are useful for the detection of cancerous cells;
 CC for the diagnosis, prognosis and management of cancer; for the
 CC identification of agents that modulate the phenotype of cancerous cells;
 CC for the identification of therapeutic targets for cancer chemotherapy;
 CC and for the treatment of cancer, especially colon cancer and metastasized
 CC colon cancer, but also breast or pancreatic cancer. The polynucleotides
 CC are also useful as a source of probes or primers for use in diagnostic
 CC methods. The differentially expressed polynucleotides or their encoded
 CC proteins can additionally be used as vaccines to modulate primary immune
 CC responses for the prevention or treatment of cancer. The present sequence
 CC represents a specifically claimed polynucleotide which is differentially
 CC expressed in colon cancer. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 624 BP; 129 A; 177 C; 148 G; 170 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 14; Length 624;

Best Local Similarity 99.3%; Pred. No. 8.7e-72;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTCTCTCCAGTGCCATGCAGT 61
 Db 153 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTCTCTCCAGTGCCATGCAGT 212
 Qy 62 TTGTCAACGTGGGGTACTTCTCATCGCAGCGCGGTTGGTCTTGGTCTTGGTTTC 121
 Db 213 TTGTCAACGTGGGGTACTTCTCATCGCAGCGCGGTTGGTCTTGGTCTTGGTTTC 272
 Qy 122 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTCAAGTTCCTTCATCC 181
 Db 273 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTCAAGTTCCTTCATCC 332
 Qy 182 TCCTCCCTCATCTTCATTGCTCAGGTTCAGTGTGCTGTGGTGCCTTGGTGTACACCAATA 241
 Db 333 TCCTCCCTCATCTTCATTGCTCAGGTTCAGTGTGCTGTGGTGCCTTGGTGTACACCAATA 392
 Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTGGTAGTGCCTGCGCATCAAGAA 287
 Db 393 TGGCTGAGCACTTCCCGACGTTGCTGTGGTAGTGCCTGCGCATCAAGAA 438

RESULT 4

AAI29471/c

ID AAI29471 standard; cDNA; 635 BP.

XX AAI29471;

XX AAI29471;

DT 12-OCT-2001 (first entry)

XX Colon tumour related determined cDNA sequence for clone R0098:P06.

XX Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;

KW gene therapy; vaccine; colonic cancer; ss.

XX Homo sapiens.

XX WO200149716-A2.

PN 12-JUL-2001.

XX

XX

PD

XX

PF 29-DEC-2000; 2000WO-US035596.

XX 30-DEC-1999; 99US-00476296.

PR 10-JAN-2000; 2000US-00480321.

PR 15-FEB-2000; 2000US-00504629.

PR 06-MAR-2000; 2000US-00519444.

PR 19-MAY-2000; 2000US-00575251.

PR 29-JUN-2000; 2000US-00609448.

XX 28-AUG-2000; 2000US-00649811.

XX (CORI-) CORIXA CORP.

XX

PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stoik JA;

PI King GE, Wang T, Jiang Y;

XX WPI; 2001-441847/47.

XX

PT Colon tumor associated proteins and nucleic acids useful for the

PT prevention, diagnosis and treatment of colonic cancer.

XX

PS Claim 2; Page 414; 472pp; English.

XX

CC The present invention describes colon tumour associated proteins (I) and

CC the polynucleotides (II) that encode them. (I) have cytostatic activity.

CC (I) and (II) can be used in gene therapy and vaccine production. (I) and

CC (II) may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate colon tumour associated protein (TCAP)

CC expression, such as colonic cancer. For example, (I) and (II) may be used

CC to treat disorders associated with decreased expression by rectifying

CC mutations or deletions in a patient's genome that affect the activity of

CC TCAPs by expressing inactive proteins or to supplement the patients own

CC production of them. Additionally, (II) may be used to produce the TCAP

CC proteins, by inserting the nucleic acids into a host cell culturing the

CC cell to express the protein. (II) and its complementary sequences may

CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)

CC and hybridization assays to detect and quantitate the presence of similar

CC nucleic acids in samples, and therefore which patients may be in need of

CC restorative therapy. (I) may also be used as antigens in the production

CC of antibodies against TCAPs and in assays to identify modulators of TCAP

CC expression and activity. Anti-(I) antibodies and antagonists may also be

CC used to down regulate TCAP expression and activity. The anti-(I)

CC antibodies may also be used as diagnostic agents for detecting the

CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbent assay

CC (ELISA)). AAI29460 to AAI29512 and AAM24494 to AAM24523 represent

CC nucleotide and amino acid sequences given in the exemplification of the

CC present invention

XX

SQ Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;

Query Match 95.2%; Score 282.8; DB 4; Length 635;

Best Local Similarity 99.3%; Pred. No. 8.8e-72;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTCTCTCCAGTGCCATGCAGT 61

Db 575 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTCTCTCCAGTGCCATGCAGT 516

Qy 62 TTGTCAACGTGGGGTACTTCTCATCGCAGCGCGGTTGGTCTTGGTCTTGGTTTC 121

Db 515 TTGTCAACGTGGGGTACTTCTCATCGCAGCGCGGTTGGTCTTGGTCTTGGTTTC 456

Qy 122 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTCAAGTTCCTTCATCC 181

Db 455 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTCAAGTTCCTTCATCC 396

Qy 182 TCCTCCTCATCTTCATTGCTCAGGTTCAGTGTGCTGTGGTGCCTTGGTGTACACCAATA 241

Db 395 TCCTCCTCATCTTCATTGCTCAGGTTCAGTGTGCTGTGGTGCCTTGGTGTACACCAATA 336

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTGGTAGTGCCTGCGCATCAAGAA 287

Db 335 TGGCTGAGCACTTCCCGACGTTGCTGTGGTAGTGCCTGCGCATCAAGAA 290

RESULT 5
ABZ33657/c
ID ABZ33657 standard; cDNA; 635 BP.
XX
XX ABZ33657;
AC
XX 30-JAN-2003 (first entry)
DT
XX
XX Human colon tumour cDNA for clone R0098:F06 SEQ ID NO:1025.
XX
XX Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200283070-A2.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 09-APR-2002; 2002WO-US011475.
PF
XX
XX 10-APR-2001; 2001US-00833263.
PR
XX 03-AUG-2001; 2001US-00922217.
PR
XX 19-DEC-2001; 2001US-00025380.
PR
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Lodes MJ, Secretist H, Benson DR, Meagher MJ, Stolk JA;
PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;
PI Fanger GR, Vedvick TS, Carter D;
XX
XX WPI; 2003-067548/06.
DR
XX
XX New polynucleotide, useful for the preparation of a composition for
PT stimulating an immune response against, or treating, cancer.
PT
XX
XX Disclosure; Page 415; 537pp; English.
PS
XX
XX The present invention describes compounds (I) for the immunotherapy and
CC diagnosis of colon cancer. Also described: (1) a method for detecting the
CC presence of cancer in a patient; (2) a method for stimulating and/or
CC expanding T cells specific for a tumour protein; (3) an isolated T cell
CC population comprising T cells prepared by the method of (2); (4) a method
CC for stimulating an immune response in a patient; (5) a method for
CC treating cancer in a patient; and (6) a method for inhibiting the
CC development of cancer in a patient. (1) have immunostimulant and
CC cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
CC and ABP55343 to ABP55391 represent human colon cancer/tumour related
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;
Query Match 95.2%; Score 282.8; DB 8; Length 635;
Best Local Similarity 99.3%; Pred. No. 8.8e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCGATGCCATGCAGT 61
DB 575 CAATCGATGGGCGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCGATGCCATGCAGT 516
QY 62 TTGTCAAGTGGGCTACTTCTTCATCGCAGCGCGGTTGTGGTCTTGTCTTGGTTCC 121
DB 515 TTGTCAAGTGGGCTACTTCTTCATCGCAGCGCGGTTGTGGTCTTGTCTTGGTTCC 456
QY 122 TGGGCTGCTATGCTGCTAAGACTGAGACGAGTGTGCCCTCGTCGAGCTTCTTTCATCC 181
DB 455 TGGGCTGCTATGCTGCTAAGACTGAGACGAGTGTGCCCTCGTCGAGCTTCTTTCATCC 396
QY 182 TCCTCCTCATCTTTCATGCTGAGGTTGACGCTGTGTGTGTCGCTTGTGTGTAACATAA 241
DB 395 TCCTCCTCATCTTTCATGCTGAGGTTGACGCTGTGTGTGTCGCTTGTGTGTAACATAA 336

QY 242 TGGCTGAGCAGCTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
DB 335 TGGCTGAGCAGCTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 290
RESULT 6
ABK29835
ID ABK29835 standard; cDNA; 792 BP.
XX
XX ABK29835;
AC
XX 23-APR-2002 (first entry)
DT
XX Colon adenocarcinoma-specific cDNA #361.
DE
XX Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.
KW
XX Homo sapiens.
OS
XX WO200196389-A2.
PN
XX
XX 20-DEC-2001.
PD
XX
XX 07-JUN-2001; 2001WO-US018574.
PF
XX 09-JUN-2000; 2000US-0210667P.
PR
XX 22-NOV-2000; 2000US-0252614P.
PR
XX (CORI-) CORIXA CORP.
PA
XX Meagher MJ, King GE, Xu J, Secretist H;
PI
XX WPI; 2002-098052/13.
DR
XX
XX New isolated polynucleotide encoding a polypeptide comprising a portion
PT of colon tumor protein, for detection, diagnosis and therapy of human
PT colon cancer.
PT
XX
XX Claim 1; Page 207; 211pp; English.
PS
XX
XX The invention relates to an isolated polynucleotide (I) encoding a
CC polypeptide (II) comprising a portion of a colon tumour protein. A new
CC oligonucleotide (III) that hybridises to (I) is useful for determining
CC the presence of a cancer in a patient. (II) or antigen presenting cells
CC expressing (I) are useful for stimulating and/or expanding T cells
CC specific for a tumour protein, by contacting T cells with (I), (II) or
CC antigen-presenting cells that express (I). (I), (II), or antigen
CC presenting cells that express (II) are useful for treating colon cancer
CC in a patient by incubating CD4+ and/or CD8+ T cells isolated from a
CC patient with (I), (II), or antigen presenting cells that express (II), so
CC that T cells proliferate, and administering to the patient an effective
CC amount of the proliferated T cells, thus inhibiting the development of a
CC cancer in the patient. A new composition is useful for stimulating an
CC immune response in a patient. (I) or (II) is useful in vaccines and
CC pharmaceutical compositions for prevention and treatment of colon cancer
CC and for the diagnosis and monitoring of the cancers. (I), (II) or an
CC antibody against (II) is useful for detection, diagnosis and/or therapy
CC of human colon cancer. (I) is useful as a probe or primer for nucleic
CC acid hybridisation, and in the design and preparation of ribozyme
CC molecules for inhibiting expression of (II) in tumour cells. ABK29475-
CC ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of
CC the invention
XX
SQ Sequence 792 BP; 165 A; 218 C; 197 G; 212 T; 0 U; 0 Other;
Query Match 95.2%; Score 282.8; DB 6; Length 792;
Best Local Similarity 99.3%; Pred. No. 9.5e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCGATGCCATGCAGT 61
DB 214 CAATCGATGGGCGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCGATGCCATGCAGT 273

CC or a drug having similar biological activity as EGFR inhibitor.
CC comprising providing a sample of tumor cells from a patient to be tested,
CC and detecting in the sample the expression of genes chosen from a panel
CC of genes (that have been correlated with sensitivity or resistance to the
CC EGFR inhibitor) and selecting the patient as being predicted to benefit
CC from therapeutic administration of the EGFR inhibitor, if the expression
CC of the gene or genes in the patient's tumor cells is statistically more
CC similar to the expression levels of the gene or genes that has been
CC correlated with sensitivity to the EGFR inhibitor than to resistance to
CC the EGFR inhibitor. Also included are identifying molecules that interact
CC with the EGFR pathway to allow or enhance responsiveness to EGFR
CC inhibitors, polynucleotides (for detecting the expression of genes that
CC are indicative of sensitivity or resistance to gefitinib, or its agonist,
CC or a drug having substantially similar biological activity as gefitinib,
CC where the polynucleotides consist of at least two polynucleotides, where
CC each polynucleotide is at least 5 nucleotides in length, and where each
CC polynucleotide is complementary to an RNA transcript, or nucleotide
CC derived from it, of a gene that is regulated differently in gefitinib-
CC sensitive tumor cells as compared to gefitinib-resistant cells),
CC antibodies (or their antigen binding fragments or peptides) for detecting
CC the expression of genes that are indicative of sensitivity or resistance
CC to gefitinib (or its agonist, or a drug having substantially similar
CC biological activity as gefitinib, which antibody selectively binds to a
CC protein encoded by a gene comprising, or expressing a transcript
CC comprising, a nucleic acid sequence appearing as AEB35137-ASB35330,
CC identifying a compound with the potential to enhance the efficacy of EGFR
CC inhibitors and treating a patient suffering from cancer. The method is
CC useful in selecting a cancer patient (especially non-small-cell lung
CC cancer) who is predicted to benefit from therapeutic administration of an
CC EGFR inhibitor or its agonist, or a drug having similar biological
CC activity as EGFR inhibitor. The present sequence represents one of the
CC 194 genes that have been correlated with sensitivity or resistance to the
CC EGFR inhibitor.

SQ Sequence 1044 BP; 220 A; 283 C; 266 G; 275 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 14; Length 1044;
Best Local Similarity 99.3%; Pred. No. 1.1e-71;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
DB 221 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 280
QY 62 TTGTCAGCTGGGCTACTTCTTCATCGACGCCGGCTGTGGTCTTTGCTCTTGTCTTCC 121
DB 281 TTGTCAGCTGGGCTACTTCTTCATCGACGCCGGCTGTGGTCTTTGCTCTTGTCTTCC 340
QY 122 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTGTGACGTTCTTCTTCATCC 181
DB 341 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTGTGACGTTCTTCTTCATCC 400
QY 182 TCTCTCTCATCTTCACTGCTGAGGTTGCGAGTGTGCTGTGCTGCCCTGTGACACCAPAA 241
DB 401 TCTCTCTCATCTTCACTGCTGAGGTTGCGAGTGTGCTGTGCTGCCCTGTGACACCA 460
QY 242 TGGCTGAGCACTCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
DB 461 TGGCTGAGCACTTCTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506

RESULT 9

ID ABS76533 standard; cDNA; 1076 BP.

XX ABS76533;

XX 11-DEC-2002 (first entry)

DE cDNA encoding human ovarian cancer marker M328.

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;
XX central nervous system disorder; bacterial meningitis; viral meningitis;

KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW brain herniation; inflammation; encephalitis; testicular disorder;
KW nontuberculous granulomatous orchitis; connective tissue disorder;
KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW histological type; carcinogenic; ovarian cancer marker; gene; ss.
OS Homo sapiens.
XX WO200271928-A2.
XX 19-SEP-2002.
XX 14-MAR-2002; 2002WO-US007826.
XX 14-MAR-2001; 2001US-0276025P.
XX 14-MAR-2001; 2001US-0276026P.
XX 10-AUG-2001; 2001US-0311732P.
XX 19-SEP-2001; 2001US-0323580P.
XX 26-SEP-2001; 2001US-0324967P.
XX 26-SEP-2001; 2001US-0325102P.
XX 26-SEP-2001; 2001US-0325149P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Monahan JB, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
XX Meyers RE, Morrissey WP, Olandt PJ, Sen A, Vieby PO, Mills GB;
XX Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX WPI; 2002-723277/78.
XX P-PSDB; ABG96434.
XX Assessing whether a patient is afflicted with ovarian cancer, useful in
XX assessing the stage or progression of the disease, comprises comparing
XX the expression level of a cancer marker in a sample from a patient and
XX from a non cancer patient.
XX Disclosure; Page 445-446; 481pp; English.
XX The present invention relates to a new method for assessing whether a
XX patient is afflicted with ovarian cancer. The method involves comparing
XX the expression level of a marker in a patient sample and the normal level
XX of expression of the marker in a control non-ovarian cancer sample, where
XX the marker is selected from 363 cancer markers described in the
XX specification. The method of the invention is useful in diagnosing or
XX characterising cancer, in detecting the presence of cancer as early as
XX possible, and the recurrence of ovarian cancer. The method may also be of
XX particular use with patients having an enhanced risk of developing
XX ovarian cancer (e.g. patients having a familial history of ovarian
XX cancer). The cancer markers may be used in the management and treatment
XX of e.g. brain and central nervous system disorders (e.g. bacterial and
XX viral meningitis, Alzheimer's disease or Parkinson's disease), brain
XX disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
XX inflammations (e.g. bacterial or viral meningitis or encephalitis),
XX testicular disorders (e.g. nontuberculous granulomatous orchitis),
XX connective tissue disorders, or heart disorders (e.g. ischaemic heart
XX disease or atherosclerosis). The compositions and methods may also be
XX used in assessing the histological type of neoplasm associated with
XX ovarian cancer, monitoring the progression of ovarian cancer, determining
XX whether ovarian cancer has metastasized or is likely to metastasize,
XX selecting a composition for inhibiting ovarian cancer, assessing the
XX ovarian carcinogenic potential of a compound, or inhibiting ovarian
XX cancer or at risk of developing ovarian cancer. The present nucleic acid
XX sequence encodes one of the ovarian cancer markers described in the
XX invention

SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 6; Length 1076;
Best Local Similarity 99.3%; Pred. No. 1.1e-71;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
|||||

Db 98 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 157
Qy 62 TTGTCAAGTGGGCTACTTCTCATCGAGCGGGTGTGTCTTTTCTGCTTTTGGTTTCC 121
Db 158 TTGTCAAGTGGGCTACTTCTCATCGAGCGGGTGTGTCTTTTCTGCTTTTGGTTTCC 217
Qy 122 TGGGCTGCTATGCTTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 218 TGGGCTGCTATGCTTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
Qy 182 TCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGCCTTGTGTACACCAATAA 241
Db 278 TCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGCCTTGTGTACACCAATAA 337
Qy 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCCTGCATCAAGAA 287
Db 338 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCCTGCATCAAGAA 383

RESULT 10

ADB75600
ID ADB75600 standard; cDNA; 1076 BP.

XX ADB75600;

XX 04-DEC-2003 (first entry)

XX Prostate cancer marker cDNA.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Homo sapiens.

XX WO2003009814-A2.

XX 06-FEB-2003.

XX 25-JUL-2002; 2002WO-US023913.

XX 25-JUL-2001; 2001US-0307982P.

XX 22-AUG-2001; 2001US-0314356P.

XX 25-SEP-2001; 2001US-0332020P.

XX 12-DEC-2001; 2001US-0341746P.

XX 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

XX Hoerish S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

XX cancer.

XX Disclosure; SEQ ID NO 424; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with
XX the cancerous state of prostate cells. Also disclosed is a method of
XX assessing whether a patient is afflicted with prostate cancer. The method
XX of the invention involves assessing whether a patient is afflicted with
XX prostate cancer by comparing the level of expression of a marker in a
XX patient sample and the normal level of expression of the marker in a
XX control non-prostate cancer sample, where a significant increase in the
XX level of expression of the marker in the patient sample and the normal
XX level indicates that the patient is afflicted with prostate cancer.
XX Nucleic acids of the invention are useful for diagnosing or treating
XX prostate cancer, and may be useful in gene therapy. Sequences given in
XX ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
Query Match 95.2%; Score 282.8; DB 10; Length 1076;
Best Local Similarity 99.3%; Pred. No. 1.1e-71;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
Db 98 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 157
Qy 62 TTGTCAAGTGGGCTACTTCTCATCGAGCGGGTGTGTCTTTTCTGCTTTTGGTTTCC 121
Db 158 TTGTCAAGTGGGCTACTTCTCATCGAGCGGGTGTGTCTTTTCTGCTTTTGGTTTCC 217
Qy 122 TGGGCTGCTATGCTTAAGACTGAGAGCAAGTGTGCCCTGCATCAAGAA 287
Db 218 TGGGCTGCTATGCTTAAGACTGAGAGCAAGTGTGCCCTGCATCAAGAA 337
Qy 182 TCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGCCTTGTGTACACCAATAA 241
Db 278 TCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGCCTTGTGTACACCAATAA 337
Qy 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCCTGCATCAAGAA 287
Db 338 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCCTGCATCAAGAA 383

RESULT 11

ADR25330
ID ADR25330 standard; DNA; 1076 BP.

XX ADR25330;

XX 21-OCT-2004 (first entry)

XX Breast cancer prognosis marker #1191.

XX ds; breast cancer; prognosis; gene expression; diagnosis.

XX Homo sapiens.

XX WO2004065545-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US001100.

XX 15-JAN-2003; 2003US-00342887.

XX (ROSE-) ROSETTA INPHARMATICS LLC.

XX (NECA-) NETHERLANDS CANCER INST.

XX Van't Veer LJ, He Y;

XX WPI; 2004-593473/57.

XX Classifying a breast cancer patient according to prognosis comprises
XX determining the similarity between the level of expression of each of
XX five genes in a cell sample taken from patient, to control levels.

XX Disclosure; SEQ ID NO 1191; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient
XX according to prognosis by determining the similarity between the level of
XX expression of each of five genes for which markers are listed in the
XX specification, in a cell sample taken from the breast cancer patient, to
XX control levels of expression for each respective five genes to obtain a
XX patient similarity value. The methods are useful for classifying a breast
XX cancer patient according to prognosis. Kits and computer program products
XX are useful for data analysis using the diagnostic, prognostic and
XX statistical methods of the invention. This sequence corresponds to a
XX marker used in the method of the invention.

SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
 Query Match 95.2%; Score 282.8; DB 13; Length 1076;
 Best Local Similarity 99.3%; Pred. No. 1.1e-71;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTCCCATGCAGT 61
 DB 98 CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTCCCATGCAGT 157
 QY 62 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGCGGTTGTGCTCTTTGCTTTGCTTTCC 121
 DB 158 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGCGGTTGTGCTCTTTGCTTTGCTTTCC 217
 QY 122 TGGGCTGCTATGCTTAAGACTGAGACAAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 181
 DB 218 TGGGCTGCTATGCTTAAGACTGAGACAAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 277
 QY 182 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGCTGCGCTTGTGTACACCAATA 241
 DB 278 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGCTGCGCTTGTGTACACCAATA 337
 QY 242 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
 DB 338 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCTGCCATCAAGAA 383

RESULT 12
 ADR65868
 ID ADR65868 standard; DNA; 1076 BP.
 XX AC ADR65868;
 XX DT 02-DEC-2004 (first entry)
 XX DE Human prostatic carcinoma derived DNA SEQ ID 64 #1.
 XX KW human; cytostatic; diagnosis; prostatic cancer;
 XX KW differential expression analysis; ds.
 XX OS Homo sapiens.
 XX PN WO2004076614-A2.
 XX PD 10-SEP-2004.
 XX PF 22-FEB-2004; 2004WO-DE000433.
 XX PR 27-FEB-2003; 2003DE-01009985.
 XX PR 14-MAY-2003; 2003DE-01022134.
 XX PA (HINZ/) HINZMANN B.
 XX PA (DAHL/) DAHL E.
 XX PA (ROSE/) ROSENTHAL A.
 XX PA (HERM/) HERMANN K.
 XX PA (PIL/) PILARSKY C.
 XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnenmann H, Roepcke S;
 PI Kinzhong L, Staub E;
 XX WPI; 2004-653386/63.
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 XX useful for diagnosis, treatment and in screening for specific binding
 XX agents.
 XX Claim 1; Page 268; 1607pp; German.
 XX This invention describes novel cytostatic polynucleotide and polypeptide
 XX sequences which can be used in a method for diagnosing prostatic cancer
 XX or the risk of developing prostatic cancer. Diagnosis is based on
 XX determining over transcription or over expression of the sequences in

CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR65954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.

SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
 Query Match 95.2%; Score 282.8; DB 13; Length 1076;
 Best Local Similarity 99.3%; Pred. No. 1.1e-71;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTCCCATGCAGT 61
 DB 98 CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTCCCATGCAGT 157
 QY 62 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGCGGTTGTGCTCTTTGCTTTGCTTTCC 121
 DB 158 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGCGGTTGTGCTCTTTGCTTTGCTTTCC 217
 QY 122 TGGGCTGCTATGCTTAAGACTGAGACAAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 181
 DB 218 TGGGCTGCTATGCTTAAGACTGAGACAAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 277
 QY 182 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGCTGCGCTTGTGTACACCAATA 241
 DB 278 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGCTGCGCTTGTGTACACCAATA 337
 QY 242 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
 DB 338 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCTGCCATCAAGAA 383

RESULT 13
 ADR66771
 ID ADR66771 standard; DNA; 1076 BP.
 XX AC ADR66771;
 XX DT 02-DEC-2004 (first entry)
 XX DE Human prostatic carcinoma derived DNA SEQ ID 64 #4.
 XX KW human; cytostatic; diagnosis; prostatic cancer;
 XX KW differential expression analysis; ds.
 XX OS Homo sapiens.
 XX PN WO2004076614-A2.
 XX PD 10-SEP-2004.

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	297	100.0	297	5	US-10-079-954-1	Sequence 1, Appli	
2	282.8	95.2	513	5	US-10-052-283-203	Sequence 203, App	
C 3	282.8	95.2	635	3	US-09-922-217-1025	Sequence 1025, Ap	
C 4	282.8	95.2	635	3	US-09-833-263-1025	Sequence 1025, Ap	
C 5	282.8	95.2	635	5	US-10-025-380-1025	Sequence 1025, Ap	
6	282.8	95.2	792	3	US-09-878-134-361	Sequence 361, App	
7	282.8	95.2	1044	8	US-10-775-920-132	Sequence 132, App	
8	282.8	95.2	1076	5	US-10-097-340-325	Sequence 325, App	
9	282.8	95.2	1076	5	US-10-205-823-424	Sequence 424, App	
10	282.8	95.2	1076	6	US-10-172-118-1191	Sequence 1191, Ap	
11	282.8	95.2	1076	7	US-10-342-887-1191	Sequence 1191, Ap	
12	282.8	95.2	1076	8	US-10-775-920-136	Sequence 136, App	
13	282.8	95.2	1076	10	US-11-051-454-424	Sequence 424, Appl	
14	282.8	95.2	1076	10	US-11-050-926-325	Sequence 325, Appl	
15	282.8	95.2	1154	5	US-10-097-340-323	Sequence 323, App	
16	282.8	95.2	1154	5	US-10-205-823-422	Sequence 422, App	
17	282.8	95.2	1154	10	US-11-051-454-422	Sequence 422, Appl	
18	282.8	95.2	1154	10	US-11-050-926-323	Sequence 323, Appl	
19	282.8	95.2	1278	6	US-10-295-027-603	Sequence 603, App	
20	282.8	95.2	1278	7	US-10-240-425-400	Sequence 400, App	
21	282.8	95.2	1278	8	US-10-775-920-130	Sequence 130, App	
22	282.8	95.2	1288	6	US-10-156-136-4	Sequence 4, Appli	
C 23	282.8	95.2	1288	6	US-10-156-136-50	Sequence 50, Appl	

	Query Match	100.0%;	Score 297;	DB 5;	Length 297;
	Best Local Similarity	100.0%;	Pred. No. 1.6e-84;		
	Matches 297;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GCAATCGATGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCACATGCAG	60		
Db	1	GCAATCGATGGGGATCCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCACATGCAG	60		
Qy	61	TTTGTCAAACGTGGGCTACTTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTC	120		
Db	61	TTTGTCAAACGTGGGCTACTTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTC	120		
Qy	121	CTGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCTGTGACGTTCTTCTTCATC	180		
Db	121	CTGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCTGTGACGTTCTTCTTCATC	180		
Qy	181	CTCCTCTCATCTTCATTGCTGAGGTTGCAAGCTGCTGTGCTCGCCTTGGGTACACCATTA	240		
Db	181	CTCCTCTCATCTTCATTGCTGAGGTTGCAAGCTGCTGTGCTCGCCTTGGGTACACCATTA	240		
Qy	241	ATGGCTGAGCACCTTCCGAGCTTGTCTGGTATGTGCTGCCATCAAGAAAGATTATGGTT	297		

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; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 618
; OTHER INFORMATION: n = A,T,C or G
US-09-922-217-1025

Query Match          95.2%; Score 282.8; DB 3; Length 635;
Best Local Similarity 99.3%; Pred. No. 6.9e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAGT 61
DB      575 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAGT 51
QY      62  TTGTCAACGTGGGCTACTTCCATCGACGGCGGTGTGGTCTTTGGCTCTTGGTTTCC 121
DB      515 TTGTCAACGTGGGCTACTTCCATCGACGGCGGTGTGGTCTTTGGCTCTTGGTTTCC 456
QY      122 TGCGGTGCTATGGTGCTAAGACTGAGACGAAGTGTGCCCTCGTGAAGTCTTCTTCAATCC 181
DB      455 TGCGGTGCTATGGTGCTAAGACTGAGACGAAGTGTGCCCTCGTGAAGTCTTCTTCAATCC 396
QY      182 TCTCTCTCATCTCATCTGCTGAGTTGCAAGTGTGCTGCTCGGCTTGGTGATACACCATAA 241
DB      395 TCTCTCTCATCTCATCTGCTGAGTTGCAAGTGTGCTGCTCGGCTTGGTGATACACCAA 336
QY      242 TGCGTGAGCACTTCCCGAGCTTGTCTGCTAGTGCTGCCATCAAGAA 287
DB      335 TGCGTGAGCACTTCTTGAGTGTGCTGCTGCCATCAAGAA 290

RESULT 4
US-09-833-263-1025/c
; Sequence 1025, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1025
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(635)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-1025

Query Match          95.2%; Score 282.8; DB 3; Length 635;
Best Local Similarity 99.3%; Pred. No. 6.9e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAGT 61
DB      575 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAGT 516
QY      62  TTGTCAACGTGGGCTACTTCCATCGACGGCGGTGTGGTCTTTGGCTCTTGGTTTCC 121

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Qy 62 TTGTCAACGCTGGGCTACTTCTCATCGCAGCCGGGTTGGTCTTTGCTCTTGGTTCC 121
Db 158 TTGTCAACGCTGGGCTACTTCTCATCGCAGCCGGGTTGGTCTTTGCTCTTGGTTCC 217
Qy 122 TGGGCTGTATGGTGCTAAGACTGAGACCAAGTGGCCCTGTCAGCTTCTTTCATCC 181
Db 218 TGGGCTGTATGGTGCTAAGACTGAGACCAAGTGGCCCTGTCAGCTTCTTTCATCC 277
Qy 182 TCCTCCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTCGCTTGGTGTCACCAATAA 241
Db 278 TCCTCCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTCGCTTGGTGTCACCAATAA 337
Qy 242 TGGCTGAGCACTTCCCGAGTTGCTGCTGAGTGGCTGCTGCCATCAAGAA 287
Db 338 TGGCTGAGCACTTCCCGAGTTGCTGCTGAGTGGCTGCTGCCATCAAGAA 383

RESULT 10

US-10-172-118-1191
; Sequence 1191, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1191
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005727
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1191

Query Match 95.2%; Score 282.8; DB 6; Length 1076;
Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 61
Db 98 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 157
Qy 62 TTGTCAACGCTGGGCTACTTCTCATCGCAGCCGGGTTGGTCTTTGCTCTTGGTTCC 121
Db 158 TTGTCAACGCTGGGCTACTTCTCATCGCAGCCGGGTTGGTCTTTGCTCTTGGTTCC 217
Qy 122 TGGGCTGTATGGTGCTAAGACTGAGACCAAGTGGCCCTGTCAGCTTCTTTCATCC 181
Db 218 TGGGCTGTATGGTGCTAAGACTGAGACCAAGTGGCCCTGTCAGCTTCTTTCATCC 277
Qy 182 TCCTCCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTCGCTTGGTGTCACCAATAA 241
Db 278 TCCTCCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTCGCTTGGTGTCACCAATAA 337
Qy 242 TGGCTGAGCACTTCCCGAGTTGCTGCTGAGTGGCTGCTGCCATCAAGAA 287
Db 338 TGGCTGAGCACTTCCCGAGTTGCTGCTGAGTGGCTGCTGCCATCAAGAA 383

RESULT 11

US-10-342-887-1191
; Sequence 1191, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1191
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1191

Query Match 95.2%; Score 282.8; DB 7; Length 1076;
Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 61
Db 98 CAATCGATGGGGCATCTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATGCAGT 157
Qy 62 TTGTCAACGCTGGGCTACTTCTCATCGCAGCCGGGTTGGTCTTTGCTCTTGGTTCC 121
Db 158 TTGTCAACGCTGGGCTACTTCTCATCGCAGCCGGGTTGGTCTTTGCTCTTGGTTCC 217
Qy 122 TGGGCTGTATGGTGCTAAGACTGAGACCAAGTGGCCCTGTCAGCTTCTTTCATCC 181
Db 218 TGGGCTGTATGGTGCTAAGACTGAGACCAAGTGGCCCTGTCAGCTTCTTTCATCC 277
Qy 182 TCCTCCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTCGCTTGGTGTCACCAATAA 241
Db 278 TCCTCCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTCGCTTGGTGTCACCAATAA 337
Qy 242 TGGCTGAGCACTTCCCGAGCTTCTGCTGAGTGGCTGCTGCCATCAAGAA 287
Db 338 TGGCTGAGCACTTCCCGAGCTTCTGCTGAGTGGCTGCTGCCATCAAGAA 383

RESULT 12

US-10-775-920-136
; Sequence 136, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Mergen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 1076
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-775-920-136

Query Match      95.2%; Score 282.8; DB 8; Length 1076;
Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACTGTGTCAGTGCATGCGAGT 61
DB 98 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACATGTGTCAGTGCATGCGAGT 157
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTCTGGTTTC 121
DB 158 TTGTCAACGTGGGCTACTTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTCTGGTTTC 217
QY 122 TGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCTGAGTGTGAGCTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 241
DB 278 TCCTCCTCATCTTCTGAGTGTGAGCTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 337
QY 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
DB 338 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCTGCCATCAAGAA 383

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RESULT 13
US-11-051-454-424
; Sequence 424, Application US/11051454
; Publication No. US20050191673A1
; GENERAL INFORMATION:
; APPLICANT: Monahan, Robert
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/11/051,454
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-454-424

Query Match      95.2%; Score 282.8; DB 10; Length 1076;
Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACATGTGTCAGTGCATGCGAGT 61
DB 98 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACATGTGTCAGTGCATGCGAGT 157
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTCTGGTTTC 121
DB 158 TTGTCAACGTGGGCTACTTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTCTGGTTTC 217
QY 122 TGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCTGAGTGTGAGCTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 241
DB 278 TCCTCCTCATCTTCTGAGTGTGAGCTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 337
QY 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
DB 338 TGGCTGAGCACTTCTGACGTTGCTGTAGTGCCTGCCATCAAGAA 383

```

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RESULT 14
US-11-050-926-325
; Sequence 325, Application US/11050926
; Publication No. US20050214831A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/11/050,926
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-926-325

Query Match      95.2%; Score 282.8; DB 10; Length 1076;

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Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2	CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT	61
Db	98	CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT	157
Qy	62	TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTTTCC	121
Db	158	TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTTTCC	217
Qy	122	TGGGCTGCTATGGTCTAAGACTGAGACCAAGTGGCCCTCGTGACGTTCTTCTCATGCC	181
Db	218	TGGGCTGCTATGGTCTAAGACTGAGACCAAGTGGCCCTCGTGACGTTCTTCTCATGCC	277
Qy	182	TCCTCTCATCTTCAATTCCTGAGGTTGAGCTGCTGCTGGTGGCTTGGTGACACCAATA	241
Db	278	TCCTCTCATCTTCAATTCCTGAGGTTGAGCTGCTGCTGGTGGCTTGGTGACACCAATA	337
Qy	242	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA	287
Db	338	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA	383

RESULT 15
US-10-097-340-323
; Sequence 323, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-323

Query Match 95.2%; Score 282.8; DB 5; Length 1154;

Best Local Similarity 99.3%; Pred. No. 8.1e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2	CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT	61
Db	221	CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT	280
Qy	62	TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTTTCC	121
Db	281	TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTTTCC	340
Qy	122	TGGGCTGCTATGGTCTAAGACTGAGACCAAGTGGCCCTCGTGACGTTCTTCTCATGCC	181
Db	341	TGGGCTGCTATGGTCTAAGACTGAGACCAAGTGGCCCTCGTGACGTTCTTCTCATGCC	400
Qy	182	TCCTCTCATCTTCAATTCCTGAGGTTGAGCTGCTGCTGGTGGCTTGGTGACACCAATA	241
Db	401	TCCTCTCATCTTCAATTCCTGAGGTTGAGCTGCTGCTGGTGGCTTGGTGACACCAATA	460
Qy	242	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA	287
Db	461	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA	506

Search completed: March 23, 2006, 12:19:21
Job time : 534 secs

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Result No.	Score	Query #			DB	ID	Description
		Match	Length				
C 1	282.8	95.2	635	12	US-11-108-172-1025	Sequence 1025, Ap	
C 2	282.8	95.2	1289	12	US-11-234-786-111	Sequence 111, App	
C 3	281.8	94.9	601	12	US-11-108-172-884	Sequence 884, App	
C 4	281.8	94.9	693	12	US-11-108-172-950	Sequence 950, App	
C 5	280.8	94.5	649	12	US-11-108-172-925	Sequence 925, App	
C 6	278	93.6	471	5	US-09-978-360A-198	Sequence 198, App	
C 7	272.8	91.9	740	12	US-11-234-786-13	Sequence 13, Appl	
C 8	263.8	88.8	729	12	US-11-234-786-17	Sequence 17, Appl	
C 9	232	78.1	479	12	US-11-108-172-472	Sequence 472, App	
C 10	220.6	74.3	801	12	US-11-234-786-16	Sequence 16, Appl	
C 11	194.8	65.6	762	12	US-11-019-711-21	Sequence 21, Appl	
C 12	191.6	64.5	751	12	US-11-234-786-11	Sequence 11, Appl	
C 13	170.8	23.8	2942	12	US-11-000-688-1103	Sequence 12, Appl	
C 14	56.6	19.1	1400	12	US-11-136-527-6335	Sequence 1103, Ap	
C 15	56.6	19.1	1497	12	US-11-136-527-2239	Sequence 6335, Ap	
C 16	51	17.2	566	7	US-10-475-075-636	Sequence 2239, Ap	
C 17	51	17.2	687	8	US-10-821-234-414	Sequence 636, App	
C 18	51	17.2	1120	8	US-10-276-233A-8	Sequence 414, App	
C 19	51	17.2	1246	12	US-11-000-688-678	Sequence 8, Appl	
C 20	49.2	16.6	1151	12	US-11-136-527-3351	Sequence 678, App	
C 21	49.2	16.6	1151	12	US-11-136-527-3351	Sequence 3351, Ap	


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; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 884
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 555
; OTHER INFORMATION: n = A,T,C or G
US-11-108-172-884

Query Match 94.9%; Score 281.8; DB 12; Length 601;
Best Local Similarity 99.0%; Pred. No. 1.7e-70;
Matches 283; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCCCATGAGT 61
Db 575 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCCCATGAGT 516
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGAGCGGGGTTGGTCTTTGCTCTTGGTTTC 121
Db 515 TTGTCAACGTGGGCTACTTCTCATCGAGCGGGGTTGGTCTTTGCTCTTGGTTTC 456
Qy 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGAGTCTTCTTCATCC 181
Db 455 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGAGTCTTCTTCATCC 396
Qy 182 TCCTCTCATCTTCATTCGAGGTTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
Db 395 TCCTCTCATCTTCATTCGAGGTTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
Qy 242 TGGCTGAGCACTTCCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
Db 335 TGGCTGAGCACTTCTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290

RESULT 4
US-11-108-172-950/c
; Sequence 950, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Mesgher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.

```

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; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 950
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 556, 676
; OTHER INFORMATION: n = A,T,C or G
US-11-108-172-950

Query Match 94.9%; Score 281.8; DB 12; Length 693;
Best Local Similarity 99.0%; Pred. No. 1.8e-70;
Matches 283; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCCCATGAGT 61
Db 576 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCCCATGAGT 517
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGAGCGGGGTTGGTCTTTGCTCTTGGTTTC 121
Db 516 TTGTCAACGTGGGCTACTTCTCATCGAGCGGGGTTGGTCTTTGCTCTTGGTTTC 457
Qy 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGAGTCTTCTTCATCC 181
Db 456 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGAGTCTTCTTCATCC 397
Qy 182 TCCTCTCATCTTCATTCGAGGTTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
Db 396 TCCTCTCATCTTCATTCGAGGTTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337
Qy 242 TGGCTGAGCACTTCCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
Db 336 TGGCTGAGCACTTCTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291

RESULT 5
US-11-108-172-925/c
; Sequence 925, Application US/11108172

```

Publication No. US20050260177A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Lodes, Michael J.
 APPLICANT: Secrist, Heather
 APPLICANT: Benson, Darin R.
 APPLICANT: Mesgher, Madeleine Joy
 APPLICANT: Stolk, John A.
 APPLICANT: Wang, Tongtong
 APPLICANT: Jiang, Yugu
 APPLICANT: Smith, Carole L.
 APPLICANT: King, Gordon E.
 APPLICANT: Wang, Aijun
 APPLICANT: Clapper, Jonathan D.
 APPLICANT: Skeiky, Yasir A. W.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Vedick Thomas S.
 APPLICANT: Carter, Darrick
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 210121.471C15
 CURRENT APPLICATION NUMBER: US/11/108,172
 PRIOR FILING DATE: 2005-04-15
 PRIOR APPLICATION NUMBER: US 10/025,380
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: US 09/922,217
 PRIOR FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: US 09/833,263
 PRIOR FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: US 09/649,811
 PRIOR FILING DATE: 2000-08-28
 PRIOR APPLICATION NUMBER: US 09/609,448
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: US 09/575,251
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/519,444
 PRIOR FILING DATE: 2000-03-06
 PRIOR APPLICATION NUMBER: US 09/504,629
 PRIOR FILING DATE: 2000-02-15
 PRIOR APPLICATION NUMBER: US 09/480,321
 PRIOR FILING DATE: 2000-01-10
 PRIOR APPLICATION NUMBER: US 09/476,296
 PRIOR FILING DATE: 1999-12-30
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1130
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 925
 LENGTH: 649
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 441..603
 OTHER INFORMATION: n = A,T,C or G

Query Match 94.5%; Score 280.8; DB 12; Length 649;
 Best Local Similarity 98.6%; Pred. No. 3.4e-70;
 Matches 282; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 CAATCGATGGGCGATCTTCTTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
 DB 576 CAATCGATGGGCGATCTTCTTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 517
 QY 62 TTGTCAAGCTGGGCTACTTCTTCATCGCAGCGGGGTTGTGCTCTTTGCTCTTGTGTTCC 121
 DB 516 TTGTCAAGCTGGGCTACTTCTTCATCGCAGCGGGGTTGTGCTCTTTGCTCTTGTGTTCC 457
 QY 122 TGGGCTGCTATGGTCTTAAGACTGAGAGAGTGGCCCTGTGAGCGTTCTTCTTCATCC 181
 DB 456 TGGGCTGCTATGGTCTTAAGACTGAGAGAGTGGCCCTGTGAGCGTTCTTCTTCATCC 397
 QY 182 TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGTCGCCCTTGGTGACACATAA 241

Db 396 TCTCTCTCACTTCATTCCTGCTGAGTTCGAGTTCGCTTGGTGGCTTGTGTACACCAAA 337
 QY 242 TGGCTGAGCACTTCCCGACCTTGTCTGTGTAGTGTCTGCTGCATCAAGAA 287
 DB 336 TGGCTGAGCACTTCCCTGACCTTGTCTGTGTAGTGTCTGCTGCATCAAGAA 291
 RESULT 6
 US-09-978-360A-198
 Sequence 198, Application US/09978360A
 Publication No. US20060009633A9
 GENERAL INFORMATION:
 APPLICANT: Edwards, Jean-Baptiste Dumas Milne
 APPLICANT: Duclert, Aymeric
 APPLICANT: Bougueleret, Lydie
 APPLICANT: Jobert, Severin
 APPLICANT: Clusel, Catherine
 TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
 FILE REFERENCE: 56 US4.CIP
 CURRENT APPLICATION NUMBER: US/09/978,360A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: US 60/066,677
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: US 60/069,957
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: US 60/074,121
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: US 60/081,563
 PRIOR FILING DATE: 1998-04-13
 PRIOR APPLICATION NUMBER: US 60/096,116
 PRIOR FILING DATE: 1998-08-10
 PRIOR APPLICATION NUMBER: US 60/099,273
 PRIOR FILING DATE: -09-04
 PRIOR APPLICATION NUMBER: US 09/191,997
 PRIOR FILING DATE: 1998-11-13
 PRIOR APPLICATION NUMBER: US 09/215,435
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: PCT/IB98/02122
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: US 09/247,155
 PRIOR FILING DATE: 1999-02-09
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 810
 SOFTWARE: Patent.pm
 SEQ ID NO 198
 LENGTH: 471
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 92..469
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 92..172
 OTHER INFORMATION: Von Heijne matrix
 OTHER INFORMATION: score 7.9
 OTHER INFORMATION: seq VVVLALGLGCGY/AK
 FEATURE:
 NAME/KEY: polyA_signal
 LOCATION: 454..459
 FEATURE:
 NAME/KEY: polyA_site
 LOCATION: 458..471
 US-09-978-360A-198

Query Match 93.6%; Score 278; DB 5; Length 471;
 Best Local Similarity 98.3%; Pred. No. 2e-69;
 Matches 281; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 CAATCGATGGGCGATCTTCTTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
 DB 39 CAATCGATGGGCGATCTTCTTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 98


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; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)-(729)
; OTHER INFORMATION: n = A,T,C or G
; US-11-234-786-13

Query Match      88.8%; Score 263.8; DB 12; Length 729;
Best Local Similarity 96.9%; Pred. No. 2.3e-65;
Matches 279; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 61
Db 221 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 280
QY 62 TTGTCAACGTGGGCTACTCTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 121
Db 281 TTGTCAACGTGGGCTACTCTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 340
QY 122 TGGGCTGCTATGTTGCTAAGACTGAGACAAAGTGTGCGCTCGTGAAGTCTTCTTCATCC 181
Db 341 TGGGCTGCTATGTTGCTAAGACTGAGACAAAGTGTGCGCTCGTGAAGTCTTCTTCATCC 400
QY 182 TCCTCTCATCTTCACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 241
Db 401 TCCTCTCATCTTCACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 459
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 289
Db 460 TGGCTGAGCACTTCCCGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 507

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RESULT 9

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US-11-108-172-472
; Sequence 472, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C15
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811

```

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; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 472
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 71, 87, 182, 218, 288, 322, 358, 386, 407, 423, 429, 473,
; LOCATION: 479
; OTHER INFORMATION: n = A,T,C or G
; US-11-108-172-472

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Query Match      78.1%; Score 232; DB 12; Length 479;
Best Local Similarity 94.6%; Pred. No. 2.3e-56;
Matches 246; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 61
Db 219 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 278
QY 62 TTGTCAACGTGGGCTACTCTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 121
Db 279 TTGTCAACGTGGGCTACTCTTCTGAAGATCTTCGGGGCCACTGTGTCGAGTCCCATGCAGT 338
QY 122 TGGGCTGCTATGTTGCTAAGACTGAGACAAAGTGTGCGCTCGTGAAGTCTTCTTCATCC 181
Db 339 TGGGCTGCTATGTTGCTAAGACTGAGACAAAGTGTGCGCTCGTGAAGTCTTCTTCATCC 398
QY 182 TCCTCTCATCTTCACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 240
Db 399 TCCTCTCATCTTCACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 458
QY 241 ATGGCTGAGCACTTCCCGAC 260
Db 459 ATGGCTGAGCACTTCCCGAC 478

```

RESULT 10

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US-11-234-786-16/c
; Sequence 16, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.

```


Qy 242 TGGCTGACCACTCCCGAGCTTGGTGTAGTGCCTGCCATCAAGAA 287
 Db 349 TGGCTGAACAATTCCTGACACTCCCTGGTGGTGCCTGTATCGAATA 394

RESULT 12

US-11-234-786-12/C
 ; Sequence 12, Application US/11234786
 ; Publication No. US20060024301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
 ; FILE REFERENCE: 210121.427C31
 ; CURRENT APPLICATION NUMBER: US/11/234,786
 ; CURRENT FILING DATE: 2005-09-23
 ; PRIOR APPLICATION NUMBER: US 09/568,857
 ; PRIOR FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: US 09/536,857
 ; PRIOR FILING DATE: 2000-05-27
 ; PRIOR APPLICATION NUMBER: US 09/483,672
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: US 09/439,313
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: US 09/352,616
 ; PRIOR FILING DATE: 1999-07-13
 ; PRIOR APPLICATION NUMBER: US 09/288,946
 ; PRIOR FILING DATE: 1999-04-09
 ; PRIOR APPLICATION NUMBER: US 09/232,149
 ; PRIOR FILING DATE: 1999-01-15
 ; PRIOR APPLICATION NUMBER: US 09/159,812
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: US 09/115,453
 ; PRIOR FILING DATE: 1998-07-14
 ; PRIOR APPLICATION NUMBER: US 09/030,607
 ; PRIOR FILING DATE: 1998-02-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 701
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 751
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(751)
 ; OTHER INFORMATION: n = A,T,C or G
 US-11-234-786-12

Query Match 64.5%; Score 191.6; DB 12; Length 751;
 Best Local Similarity 87.7%; Pred. No. 7,5e-45;
 Matches 257; Conservative 0; Mismatches 29; Indels 7; Gaps 5;
 Qy 2 CAATGATGGGCATCCCTTTCTGAAGATCTTCGGG---CCACTGTCGTCAGTGCATGC 58
 Db 581 CAATNGATGGGCATCCCTTTTGAAGATTTTNGGCCCACTGTGGNTCCCAATGCCATGC 522
 Qy 59 -AGTTTGTCAACGCTGGGCT-ACTTCTCATCGACCGCGGTTGTGGTCTTTGCTCTTGG 116

Db 521 AGTTTGTCAACGNGGGTNAATTTCTTCATCGACCGGNGTGTGCTCTTNTNTTGG 462
 Qy 117 -TTTCTGGGCTGCTATGTTGCTAAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCT 175
 Db 461 TTTTCANGGGCTGNTATGGTGTAAAGACTGAGAGCAAGTGTGCCCTCGACGTTCTTCT 402
 Qy 176 TCATCTCTCTCTCATCTTCATTTGCTGAGCTTGCAGCTGCTGTGGTGCCTTGGTGTACA 235
 Db 401 TCATCTCTCTCTCATCTTCATTTGCTGAGTNGAGCTGCTGTGGTGCCTTGGTGTACA 342
 Qy 236 CCATAATGGCTGAGCACTTCCC-GACGTTGCTGTGTAGTGCCTGTCATCAAGAA 287
 Db 341 CCACATGGCTGAGCACTTCCCTGACGTTGCTGTGTAGTGCCTGTCATCAAGAA 289

RESULT 13

US-11-000-688-1103
 ; Sequence 1103, Application US/11000688
 ; Publication No. US20050287544A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERTUCCI, Francois
 ; APPLICANT: HOULGATTE, Remi
 ; APPLICANT: BIRNBAUM, Daniel
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
 ; FILE REFERENCE: 1423-R-03
 ; CURRENT APPLICATION NUMBER: US/11/000,688
 ; CURRENT FILING DATE: 2004-12-01
 ; PRIOR APPLICATION NUMBER: US 60/525,987
 ; PRIOR FILING DATE: 2003-12-01
 ; NUMBER OF SEQ ID NOS: 1596
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1103
 ; LENGTH: 2942
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial sequences:primer
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(2942)
 ; OTHER INFORMATION: tetraspanin similar to uroplakin
 ; OTHER INFORMATION: 1(LOC90139) gene.
 US-11-000-688-1103

Query Match 23.8%; Score 70.8; DB 12; Length 2942;
 Best Local Similarity 62.4%; Pred. No. 2e-10;
 Matches 111; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
 Qy 58 CAGTTTGTCAACGTTGGGCTACTTCTCATCGACCGCGTGTGGTCTTTTGTCTTTGGT 117
 Db 196 CTGCTCTCTACGGGCGCTTACATCTCTGCGCATGGGGCGCTCTTTCTGCTCGGC 255
 Qy 118 TTCCTGGGCTGCTATGTTGCTAAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCTTC 177
 Db 256 TTCCTGGGCTGCTGCGGGCGGCTCCGTGAGAACAAAGTGTCTGCTGCTATTTTCTCTCG 315
 Qy 178 ATCTCTCTCTCATCTTCATTTGCTGAGTTCAGCTGCTGTGGTGCCTTGGTGTACA 235
 Db 316 TTCACTCTGATCATCTTCTTCTGGCAGAGCTCTCAGACGCCATCTCTGGGCTTCATCTTCA 373

RESULT 14

US-11-136-527-6335
 ; Sequence 6335, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25

```

/ / PRIOR APPLICATION NUMBER: US 60/574,294
/ /
/ / PRIOR FILING DATE: 2005-05-26
/ /
/ / NUMBER OF SEQ ID NOS: 362830
/ /
/ / SOFTWARE: PatentIn version 3.2
/ /
/ / SEQ ID NO 6335
/ /
/ / LENGTH: 1400
/ /
/ / TYPE: DNA
/ /
/ / ORGANISM: Rattus norvegicus
/ /
/ / FEATURE:
/ /
/ / NAME/KEY: misc feature
/ /
/ / LOCATION: (1093)..(1093)
/ /
/ / OTHER INFORMATION: n is a, c, g, or t
/ /
/ / FEATURE:
/ /
/ / NAME/KEY: misc_feature
/ /
/ / LOCATION: (1390)..(1390)
/ /
/ / OTHER INFORMATION: n is a, c, g, or t
/ /
/ / US-11-136-527-6335

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	Query Match	19.1%;	Score 56.6;	DB 12;	Length 1400;
	Best Local Similarity	59.0%;	Pred. No. 1.8e-06;		
	Matches	95;	Conservative	1;	Mismatches 65;
					Indels 0; Gaps 0;
QY	75	CTACTTCTCATCGACGCGGTGTGCTTTGCTCTGTGGTTCTCGGGCGCTATGG	134		
Db	311	CTAATTCTCATTTGCTGGGAGCTGTGATGAATTTGTAGGCTTCTCGGGTGTCTATGG	370		
QY	135	TGCTAAGACTGAGCAAGTGTGCCCTCGTGCAGCTTCTTTTCATCTCTCTCATCTT	194		
Db	371	GGCCATCCAGGAGTCCCAAGTGCCTGCTGGGGAGGTCTTTCAC TTGCCTTGTGATCCTGTT	430		
QY	195	CATTGCTGAGGTTGCAGCTGCTGTGGTTCGCCTTGGGTACA	235		
Db	431	TGCCTGTGAGGTAGCTGCGGGCATCTGGGGCTTTGTAAACA	471		

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RESULT 15
US-11-136-527-2239
; Sequence 2239, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMJ01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2239
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1190)..(1190)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1487)..(1487)
; OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-2239

```

[illegible]

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:40:14 ; Search time 4.09839 Seconds
(without alignments)
1394.518 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

Sequence: 1 gcaatgatgggcatcctt.....ccatcaagaagattatggtt 297

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/abs/ABSSWEB-spool/US10079954/runat_23032006_102931_1829/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10079954.QCGN.1.1.77 @runat_23032006_102931_1829 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DRV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	453	80.3	241	2	A59262 tetraspan TSPAN-1
2	149.5	26.5	238	2	A59265 tetraspan TSPAN-4
3	146.5	26.0	219	1	A39574 leukocyte antigen
4	141	25.0	236	1	A35649 cell surface prote
5	141	25.0	236	1	A46472 cell surface prote
6	137.5	24.4	237	1	A36056 tumor-associated a
7	132	23.4	226	1	JX0221 CD9 antigen - bovi
8	131	23.2	226	1	S39262 CD9 antigen - rat
9	131	23.2	226	2	I49589 antigen - mouse
10	131	23.2	253	2	A59264 tetraspan TSPAN-3
11	130.5	23.1	219	1	A37243 hemopoietic cell s
12	130	23.0	228	1	A40402 CD9 antigen [valid
13	130	23.0	228	1	A42929 CD9 antigen - gree
14	130	23.0	282	2	T21696 hypothetical prote

15	129.5	23.0	267	1	A46493 metastasis suppres
16	129	22.9	218	1	A43522 23K integral membr
17	127.5	22.6	222	2	A59263 tetraspan TSPAN-2
18	127.5	22.6	266	2	C33/R2/IA4 - mouse
19	127	22.5	218	1	A40181 23K integral membr
20	125	22.2	238	1	I38016 melanoma-associate
21	114	20.2	238	1	JC2297 CD63 antigen - rab
22	112	19.9	238	1	A46508 CD63/ME491 antigen
23	112	19.9	238	1	S43511 CD63/ME491 antigen
24	107	19.0	194	2	T25548 hypothetical prote
25	105.5	18.7	281	1	B47629 cell surface glyco
26	105	18.6	242	2	T15361 hypothetical prote
27	104	18.4	233	2	T15620 hypothetical prote
28	103.5	18.4	245	2	A59258 tetraspan TSPAN-6
29	100.5	17.8	245	2	A59260 tetraspan TSPAN-6
30	92.5	16.4	264	2	A59261 tetraspan TSPAN-5
31	92.5	16.4	281	1	A47629 cell surface glyco
32	92	16.3	1711	2	C71625 variant-specific s
33	91	16.1	244	2	T13615 hypothetical prote
34	87	15.4	244	1	I39368 T-cell acute lymph
35	87	15.4	308	2	T24912 hypothetical prote
36	84	14.9	223	2	T26763 hypothetical prote
37	83	14.7	309	2	T34080 hypothetical prote
38	81	14.4	162	2	T52593 NADH2 dehydrogenas
39	78	13.8	208	2	S72368 homeobox protein H
40	77.5	13.7	779	2	G84561 hypothetical prote
41	77	13.7	209	2	AB3362 multiple antibioti
42	77	13.7	1992	1	S02771 myosin heavy chain
43	76.5	13.6	204	2	D91120 probable oxidoredu
44	76.5	13.6	204	2	D85965 probable oxidoredu
45	76.5	13.6	209	2	H65092 hypothetical prote

ALIGNMENTS

RESULT 1

A59262
tetraspan TSPAN-1 - human
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59262
R: Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A:Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
A:Reference number: A59258; MUID:98390278; PMID:9714763
A:Accession: A59262
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-241 <TOD>
A:Cross-references: UNIPROT:O60635; UNIPARC:UPI0000004EE36; GB:AF054838; NID:92997740; P1:
C:Genetics:
A:Gene: TSPAN-1
C:Superfamily: CD9 antigen

Alignment Scores:
Pred. No.: 2.38e-39 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 2 Gaps: 0

US-10-079-954-1 (1-297) x A59262 (1-241)

Qy	1	GCATCATGGGCGCATCTTCTGAGATCTTGGGCGACTGCTCCAGTCCATGCATGCAG	60
Db	33	SerileaspGlyAlaSerPheLeuLysilePheGlyProleuSerSerAlaMetGln	52
Qy	61	TTTGTCAACGTGGGCTACTTCTCATCGACCGCGCTTGTGGTCTTGTCTTGTGTTTC	120
Db	53	PheValIasnValGlyTyrPheLeulleAlaAlaGlyValValPheAlaLeuGlyPhe	72
Qy	121	CTGGGCTGTATGGTGCTAAGACTTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC	180

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Db 73 LeuGlyCybYrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe112
|||
Qy 181 CTCCTCTCATCTTCATTGCTGAGGTTGCAGCTGCTGGTGGCGCTTGATACACCATTA 240
|||
Db 93 LeuLeuLeuLeuPheAlaGluValAlaAlaValAlaLeuValThrThr 112
|||
Qy 241 ATGGCTGAGCACTCCCGACGTTGCTGTAGTGCCTGCATCAAGAG 288
|||
Db 113 MetAlaGluHisPheLeuThrLeuValValProAlaIleLysLys 128
|||
RESULT 2
A39574
tetraspan TSPAN-4 - human
C:Species: Homo sapiens (man)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59265
R: Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A:Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
A:Reference number: A59258; MUID:98390278; PMID:9714763
A:Accession: A59265
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-238 <TD>
A:Cross-references: UNIPROT:O14817; UNIPARC:UPI000013683P; GB:AF054841; NID:G2997746; P1
C:Genetics:
A:Gene: TSPAN-4
C:Superfamily: CD9 antigen
Alignment Scores:
Pred. No.: 1.52e-07 Length: 238
Score: 149.50 Matches: 31
Percent Similarity: 60.9% Conservative: 11
Best Local Similarity: 44.9% Mismatches: 26
Query Match: 26.5% Indels: 1
DB: 2 Gaps: 1
US-10-079-954-1 (1-297) x A59265 (1-238)
Qy 31 TTGGGGCCACTGCTCCAGTGCCATGCAGTTGTCAACGTGGCTACTCTCATCGCA 90
|||
Db 41 PheAlaThrLeuSerSerSer---PheProSerLeuSerAlaAlaLeuLeuIle 59
|||
Qy 91 GCGGCGTTGGTCTTTGCTGCTGGTCTGGTCTGGCTGCTATGGTGAAGCTGAGAGC 150
|||
Db 60 ThrGlyAlaPheValMetAlaIleGlyPheValGlyCysLeuGlyAlaIleLysGluAsn 79
|||
Qy 151 AAGTGTGCGCTGCTGCTGCTCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 210
|||
Db 80 LysCysLeuLeuThrPhePheLeuLeuLeuLeuValPheLeuLeuGluAlaThr 99
|||
Qy 211 GCTGCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 237
|||
Db 100 IleAlaIleLeuPhePheAlaThrThr 108
|||
RESULT 3
A39574
leukocyte antigen OX-44 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Aug-1991 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A39574
R: Bellacosa, A.; Lazo, P.A.; Bear, S.E.; Tsichlis, P.N.
Mol. Cell. Biol. 11, 2864-2872, 1991
A:Title: The rat leukocyte antigen MRC OX-44 is a member of a new family of cell surface
A:Reference number: A39574; MUID:91203909; PMID:2017181
A:Accession: A39574
A:Molecule type: mRNA
A:Residues: 1-219 <BEU>
A:Cross-references: UNIPROT:P24485; UNIPARC:UPI000004F1F0; GB:M57276; NID:G205897; PIDN:
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
P:1-10/Domain: intracellular #status predicted <CV1>
```

```
F:11-36/Domain: transmembrane #status predicted <TM1>
F:37-54/Domain: extracellular #status predicted <EX1>
F:55-73/Domain: transmembrane #status predicted <TM2>
F:74-79/Domain: intracellular #status predicted <CY2>
F:80-106/Domain: transmembrane #status predicted <TM3>
F:107-181/Domain: extracellular #status predicted <EX2>
F:182-204/Domain: transmembrane #status predicted <TM4>
F:205-219/Domain: intracellular #status predicted <CY3>
F:119,129,148/Binding site: carbohydrate (Asn) (covalent) #status predicted
Alignment Scores:
Pred. No.: 3.16e-07 Length: 219
Score: 146.50 Matches: 28
Percent Similarity: 64.3% Conservative: 17
Best Local Similarity: 40.0% Mismatches: 20
Query Match: 26.0% Indels: 5
DB: 1 Gaps: 1
US-10-079-954-1 (1-297) x A39574 (1-219)
Qy 55 ATGCAGTTTGTCAACGTGGGCTACTCTCATCGACCGCGCTGTGGTCTTTGCTCTT 114
|||
Db 47 LeuProPheLeuThrLeuGlyAsnValLeuValLeuValGlySerIleIleMetValVal 66
|||
Qy 115 GGTTCCTCGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCCCTCGTACGCTTCTTC 174
|||
Db 67 AlaPheLeuGlyCysMetGlySerIleLysGluAsnLysCysLeuLeuMetSerPhePhe 86
|||
Qy 175 TTCATCTCTCTCTCATCTTCATTGCTGAGTTGCAGCTGCTGTGGTGGCTGGTGTAC 234
|||
Db 87 ValLeuLeuLeuLeuLeuLeuAlaGluValThrLeuAlaIleLeuLeuPheValThr 106
|||
Qy 235 -----ACCAATAATGGCTGAG 249
|||
Db 107 GluLysLysIleAsnThrLeuValAlaGlu 116
|||
RESULT 4
A35649
cell surface protein TAPA-1 - human
N:Alternate names: target of antiproliferative antibody (TAPA) 1
C:Species: Homo sapiens (man)
C>Date: 28-Sep-1990 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A35649
R: Oren, R.; Takahashi, S.; Doss, C.; Levy, R.; Levy, S.
Mol. Cell. Biol. 10, 4007-4015, 1990
A:Title: TAPA-1, the target of an antiproliferative antibody, defines a new family of tr
A:Reference number: A35649; MUID:90318365; PMID:1695320
A:Accession: A35649
A:Molecule type: mRNA
A:Residues: 1-236 <ORF>
A:Cross-references: UNIPROT:P60033; UNIPARC:UPI0000047033; GB:M33680; NID:G338677; PIDN:
C:Genetics:
A:Gene: GDB:TAPA1
A:Cross-references: GDB:I35038; OMIM:186845
A:Map position: 11p15.5-11p15.5
C:Superfamily: CD9 antigen
C:Keywords: transmembrane protein
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-57/Domain: extracellular #status predicted <EX1>
F:58-84/Domain: transmembrane #status predicted <TM2>
F:85-88/Domain: intracellular #status predicted <CY2>
F:89-113/Domain: transmembrane #status predicted <TM3>
F:114-203/Domain: extracellular #status predicted <EX2>
F:204-230/Domain: transmembrane #status predicted <TM4>
F:231-236/Domain: intracellular #status predicted <CY3>
Alignment Scores:
Pred. No.: 1.19e-06 Length: 236
Score: 141.00 Matches: 28
Percent Similarity: 67.3% Conservative: 7
Best Local Similarity: 53.8% Mismatches: 17
Query Match: 25.0% Indels: 0
```

R;Szala, S.; Kasai, Y.; Steplewski, Z.; Rodeck, U.; Koprowski, H.; Linnenbach, A.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6833-6837, 1990
A;Title: Molecular cloning of cDNA for the human tumor-associated antigen CO-029 and ide
A;Reference number: A36056; MUID:90370878; PMID:2395876
A;Accession: A36056
A;Molecule type: mRNA
A;Residues: 1-237 <SA>
A;Cross-references: UNIPROT:P19075; UNIPARC:UPI000003BE40; GB:M35252; NID:g180925; PIDN:
C;Genetics:
A;Gene: GDB:TW4SF3
A;Cross-references: GDB:9113496; OMIM:600769
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-33/Domain: transmembrane #status predicted <TM1>
F;34-52/Domain: extracellular #status predicted <EX1>
F;53-76/Domain: transmembrane #status predicted <TM2>
F;79-82/Domain: intracellular #status predicted <CY2>
F;83-107/Domain: transmembrane #status predicted <TM3>
F;108-205/Domain: extracellular #status predicted <EX2>
F;206-232/Domain: transmembrane #status predicted <TM4>
F;233-237/Domain: intracellular #status predicted <CY3>
F;37,118/Binding site: carbohydrate (Asn) #status predicted

Alignment Scores:
Pred. No.: 2,76e-06 Length: 237
Score: 137.50 Matches: 30
Percent Similarity: 59.4% Conservative: 11
Best Local Similarity: 43.5% Mismatches: 27
Query Match: 24.4% Indels: 1
DB: 1 Gaps: 1

US-10-079-954-1 (1-297) x A36056 (1-237)

QY 28 ATCTTCGGGCCACTGTCTGTCAGTGCATGCTTGTTCACGTGGCTACTTCTCTCATC 87
Db 42 ILEPHEGLYSERGLUASPVALGLYSERSEPTYRVALALVALASP---ILEULLE 60
QY 88 GCAGCGCGGCTGTGGTCTTTGGCTTGTCTTCTTCTTCCTGGGCTGCTATGGTCTAAGACTGAG 147
Db 61 ALAVALGLYALALLEILEMETILEULGLYPHELEUGLYCYSCYSGLYALALLELYSGLU 80
QY 148 AGCAAGTGTCCCTCGTGCAGCTTCTTCTTCATCTCTCTCTCATCTCTCTCATCTTCATTGCTGAGGTT 207
Db 81 SERARGCYSMETLEULEULEULEUPHEPHEILEGLYLEULEULEULEULEULEULEULEULE 100
QY 208 GCAGCTGCTGTGGTGGCTGGCTGGCTGTAC 234
Db 101 ALATHRGLYLEULEUGLYALALVALPHE 109

RESULT 7
JX0221
CD9 antigen - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: JX0221
R;Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell.
A;Reference number: JX0221; MUID:93054422; PMID:1339429
A;Accession: JX0221
A;Molecule type: mRNA
A;Residues: 1-226 <VAR>
A;Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:g162820; PIDN:
A;Experimental source: ocular ciliary epithelial cell
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-26/Product: CD9 antigen #status predicted <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>

F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1,69e-05 Length: 228
Score: 130.00 Matches: 26
Percent Similarity: 68.8% Conservatives: 7
Best Local Similarity: 54.2% Mismatches: 15
Query Match: 23.0% Indels: 0
DB: 1 Gaps: 0

US-10-079-954-1 (1-297) x A40402 (1-228)

Qy 76 TACTTCTCATCGACGCGGCTGTGCTTTGCTCTGTGTTCTCGGCTCATGGT 135
Db 61 TyrilleuileGlyAlaGlyAlaLeuMetMetLeuValGlyPheLeuGlyCysGly 80
Qy 136 GCTAGACTGAGACGAGTGTGCTCGTGTGCTCTTCTTCTCATCTCTCTCTCTCT 195
Db 81 AlalValGlnSerGlnCysMetLeuGlyLeuPhePheGlyPheLeuValVallePhe 100
Qy 196 ATTGCTGAGTGTGCTGCTGTG 219
Db 101 AlalleGluileAlaAlaAlaile 108

RESULT 13

A42929
CD9 antigen - green monkey
N:Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A42929
R:Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
ceptors on toxin-sensitive cells.
A:Reference number: A42929; MUID:92394967; PMID:1522113
A:Accession: A42929
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-228 <MT>
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:9218565; PIDN:
C:Superfamily: CD9 antigen

C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:52.53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1,69e-05 Length: 228
Score: 130.00 Matches: 26
Percent Similarity: 68.8% Conservatives: 7
Best Local Similarity: 54.2% Mismatches: 15
Query Match: 23.0% Indels: 0
DB: 1 Gaps: 0

US-10-079-954-1 (1-297) x A42929 (1-228)

Qy 76 TACTTCTCATCGACGCGGCTGTGCTTTGCTCTGTGTTCTCGGCTCATGGT 135
Db 61 TyrilleuileGlyAlaGlyAlaLeuMetMetLeuValGlyPheLeuGlyCysGly 80

Qy 136 GCTAGACTGAGACGAGTGTGCTCGTGTGCTCTTCTTCTCATCTCTCTCTCTCT 195
Db 81 AlalValGlnSerGlnCysMetLeuGlyLeuPhePheGlyPheLeuValVallePhe 100
Qy 196 ATTGCTGAGTGTGCTGCTGTG 219
Db 101 AlalleGluileAlaAlaAlaile 108

RESULT 14

T21696
hypothetical protein F33C8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21696
R:Percy, C.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z19460
A:Accession: T21696
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-282 <MT>
A:Cross-references: UNIPROT:Q19983; UNIPARC:UPI000004EE37; EMBL:Z69790; PIDN:CAA93655.1;
A:Experimental source: clone F33C8
C:Genetics:
A:Gene: CESP:F33C8.3
A:Map position: X
A:Introns: 20/3; 51/1; 88/3; 146/3; 197/1; 235/3
C:Superfamily: CD9 antigen

Alignment Scores:
Pred. No.: 1,67e-05 Length: 282
Score: 130.00 Matches: 29
Percent Similarity: 52.6% Conservatives: 12
Best Local Similarity: 37.2% Mismatches: 29
Query Match: 23.0% Indels: 8
DB: 2 Gaps: 1

US-10-079-954-1 (1-297) x T21696 (1-282)

Qy 10 GGGGCATCTTTCGAGATCTTCGGGCCACTTCGGCCACTGTGTCAGTGCCATG----- 57
Db 28 GlyLeuGlyIleTrpLeuLeuPheAspProAlaAlaSerAaspPheAlaLeuHisSer 47
Qy 58 -----CAGTTTGCACGGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 105
Db 48 ThrHisProGlyAlaPheArgTyrValGlyTrpPheLeuValGlyAlaGlyAlaIle 67
Qy 106 TTGTCTTGTGTTCTCGGCTGTGCTGTGCTAAGACTGAGAGCAAGTGTGCTCGT 165
Db 68 IleLeuValGlyTyrPheGlyCysIleGlyAlaTrpLysMetAaGlnCysAlaLeuAla 87
Qy 166 AGTTTCTTCT 219
Db 88 PhePheCysCysIleLeuLeuAlaPhePheLeuGluLeuAlaAlaAlaVal 105

RESULT 15

A46493
metastasis suppressor KAI1 - human
N:Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible; type
C:Species: Homo sapiens (man)
C>Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: I38942; S16156; R46493
R:Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, J.
Science 268, 884-886, 1995
A:Title: KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 11p1
A:Reference number: I38942; MUID:95273964; PMID:7754374
A:Accession: I38942
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-267 <RES>
A:Cross-references: UNIPROT:P27701; UNIPARC:UPI00001273AE; EMBL:U20770; NID:9806805; PIDN:
R:Gaugitsch, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.

Bur. J. Immunol. 21, 377-383, 1991
 A:Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homolog
 A:Reference number: S16156; MUID:91153380; PMID:1842498
 A:Accession: S16156
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-267 <GAU>
 A:Cross-references: UNIPARC:UPI00001273AE; EMBL:X53795; NID:g35832; PIDN:CAA37804.1; PID
 A:Note: the authors translated the codon AGC for residue 50 as Thr
 R:Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, M
 J. Immunol. 149, 2879-2886, 1992
 A:Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell leuk
 D9, CD37, CD53, and CD63.
 A:Reference number: A46493; MUID:93017900; PMID:1401919
 A:Accession: A46493
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-239, MV, 242-267 <IMA>
 A:Cross-references: UNIPARC:UPI000016B3A0; GB:S48196; NID:g258294; PIDN:AAB23825.1; PID:
 A:Experimental source: T-cell line MOLT-4
 A:Note: sequence extracted from NCBI backbone (NCBIP:117149)
 C:Genetics:
 A:Gene: GDB:XA11

A:Cross-references: GDB:134216; OMIM:600623
 A:Map position: lip11.2-lip11.2
 C:Superfamily: CD9 antigen
 C:Keywords: Glycoprotein; transmembrane protein
 F:1-10/Domain: intracellular #status predicted <CY1>
 F:11-36/Domain: transmembrane #status predicted <TM1>
 F:37-57/Domain: extracellular #status predicted <EX1>
 F:58-78/Domain: transmembrane #status predicted <TM2>
 F:79-83/Domain: intracellular #status predicted <CY2>
 F:84-108/Domain: transmembrane #status predicted <TM3>
 F:109-227/Domain: transmembrane #status predicted <TM4>
 F:228-252/Domain: extracellular #status predicted <EX2>
 F:253-265/Domain: transmembrane #status predicted <TM4>
 F:129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

Pred. No.:	1-89e-05	Length:	267
Score:	129.50	Matches:	34
Percent Similarity:	53.7%	Conservative:	10
Best Local Similarity:	41.5%	Mismatches:	31
Query Match:	23.0%	Indels:	7
DB:	1	Gaps:	3

US-10-079-954-1 (1-297) x A46493 (1-267)

QY	7	GATGGGCGATCTTTCTGAAGATCTTCGGGCACCTGCTGCAGTGCCATGCGAGTTTGTC	66
Db	37	AspLysSerSerPheIleSerValLeuGlnThrSerSerSerSer-----Leu	52
QY	67	AACGTGGGG---TACTTCCTCATCCGAGCGCGGTGGTCTTGGCTCTGGTTCTCTG	123
Db	53	ArgMetGlyAlaTyrValPheIleGlyValGlyAlaValThrMetLeuMetGlyPheLeu	72
QY	124	GGCTGCTATGGTGAAGACTGCAGAGCAAGTGCCTCGTGCAGCTTCTTTCATCCTC	183
Db	73	GlyCysIleGlyAlaValAsnGluValArgCysLeuLeuGlyLeuTyrPheAlaPheLeu	92
QY	184	CTCCTCATCTTCGTCGAGGTTCGAGCTGCTGTGGTGGCTGTACACCAATATG	243
Db	93	LeuLeuIleLeuIleAlaGlnValThrAlaGly-----AlaLeuPheTyrPheAsnMet	110
QY	244	GCTGAG	249
Db	111	GlyLys	112

Search completed: March 23, 2006, 12:47:13
 Job time : 22.4919 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 11:29:26 ; Search time 2439 Seconds
(without alignments)
5697.320 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 297

Sequence: 1 gcaatcgatgggcacccctt.....ccatcaagaagattatgggtt 297

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gsl1:*

10: gb_gsl2:*

11: gb_gsl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283.2	95.4	777	CF595432	AGENCOURT
2	282.8	95.2	518	CB161656	K-EST0221
3	282.8	95.2	539	CD709223	EST25750
4	282.8	95.2	542	BM819747	K-EST0087
5	282.8	95.2	543	BM819711	K-EST0087
6	282.8	95.2	546	CD700012	EST16536
7	282.8	95.2	549	BE249898	E00942941
8	282.8	95.2	554	BM819756	K-EST0087
9	282.8	95.2	559	BK480177	DKFZp866E
10	282.8	95.2	564	BG428609	602494743
11	282.8	95.2	566	BM819724	K-EST0087
12	282.8	95.2	568	BM819713	K-EST0087
13	282.8	95.2	568	BP262643	BP262643
14	282.8	95.2	571	BM819701	K-EST0087
15	282.8	95.2	571	BP262874	BP262874
16	282.8	95.2	573	BP263326	BP263326
17	282.8	95.2	576	BP260827	BP260827
18	282.8	95.2	579	CD701289	EST17813
19	282.8	95.2	581	BP254783	BP254783
20	282.8	95.2	581	BP262395	BP262395
21	282.8	95.2	582	BP260782	BP260782
22	282.8	95.2	582	BP261111	BP261111

23	282.8	95.2	582	3	BP263686	BP263686
24	282.8	95.2	582	3	BP263741	BP263741
25	282.8	95.2	582	3	BP276804	BP276804
26	282.8	95.2	582	3	BP330600	BP330600
27	282.8	95.2	582	3	BP330653	BP330653
28	282.8	95.2	582	3	BP330738	BP330738
29	282.8	95.2	582	3	BP330807	BP330807
30	282.8	95.2	582	6	CD698393	EST14916
31	282.8	95.2	583	3	BM819683	BM819683 K-EST0087
32	282.8	95.2	583	3	BP255135	BP255135
33	282.8	95.2	583	3	BP260638	BP260638
34	282.8	95.2	583	3	BP262132	BP262132
35	282.8	95.2	583	3	BP342136	BP342136
36	282.8	95.2	584	3	BP263144	BP263144
37	282.8	95.2	585	3	BP331321	BP331321
38	282.8	95.2	585	6	CB216655	NISC nc07
39	282.8	95.2	586	3	BM836692	BM836692 K-EST0112
40	282.8	95.2	601	3	BM819685	BM819685 K-EST0087
41	282.8	95.2	604	6	CD704563	CD704563 EST21090
42	282.8	95.2	610	6	CD699899	CD699899 EST16423
43	282.8	95.2	613	3	BM828457	BM828457 K-EST0101
44	282.8	95.2	614	6	CD691226	CD691226 EST7749 h
45	282.8	95.2	622	6	CD698114	CD698114 EST14637

ALIGNMENTS

RESULT 1
CF595432

LOCUS

DEFINITION

AGENCOURT 15657387 NCI CGAP St3 Homo sapiens cDNA clone

IMAGE:30703089 5', mRNA sequence.

ACCESSION

CF595432

VERSION

CF595432.1 GI:36350884

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 777)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: ggapbs-x@mail.nih.gov

Tissue Procurement: Arnold Schwartz, MD, PhD

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: NDCW249 row: p column: 10

High quality sequence stop: 453.

Location/Qualifiers

1. 777

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30703089"

/tissue_type="Stomach, adenocarcinoma"

/lab_host="DH10B (tr1 phage-resistant)"

/clone_lib="NCI CGAP St3"

/notes="Vector: pDNR-LIB; Site 1: Sfil (ggccattatggcc);

Site 2: Sfil (ggccctctggcc); Library is oligo-dT primed

and directionally cloned. 5' and 3' adaptors were used in

cloning as follows: 5' adaptor sequence:

5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:

CF595432 777 bp mRNA linear EST 26-SEP-2003
IMAGE:30703089 5', mRNA sequence.

CF595432

CF595432.1 GI:36350884

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 777)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: ggapbs-x@mail.nih.gov

Tissue Procurement: Arnold Schwartz, MD, PhD

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Clone distribution: Agencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: NDCW249 row: p column: 10

High quality sequence stop: 453.

Location/Qualifiers

1. 777

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30703089"

/tissue_type="Stomach, adenocarcinoma"

/lab_host="DH10B (tr1 phage-resistant)"

/clone_lib="NCI CGAP St3"

/notes="Vector: pDNR-LIB; Site 1: Sfil (ggccattatggcc);

Site 2: Sfil (ggccctctggcc); Library is oligo-dT primed

and directionally cloned. 5' and 3' adaptors were used in

cloning as follows: 5' adaptor sequence:

5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGGCGGCGGCGCATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.30 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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ORIGIN
Query Match      95.4%; Score 283.2; DB 6; Length 777;
Best Local Similarity 99.0%; Pred. No. 3.2e-68;
Matches 285; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
    |||
Db 241 CAATCGATGGGCGATCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 300

Qy 62 TTGTCAAGCTGGGCTACTTCTCATCGAGCGCGGCTTGTGCTCTTGTCTTCTTGTTC 121
    |||
Db 301 TTGTCAAGCTGGGCTACTTCTCATCGAGCGCGGCTTGTGCTCTTGTCTTCTTGTTC 360

Qy 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGACGTTCTTTCATCC 181
    |||
Db 361 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGACGTTCTTTCATCC 420

Qy 182 TCCTCTCATCTTCAATGCTGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
    |||
Db 421 TCCTCTCATCTTCAATGCTGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Qy 242 TGGCTGAGCAGCTTCCGAGCTTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 289
    |||
Db 481 TGGCTGAGCAGCTTCCGAGCTTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 528

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RESULT 2
LOCUS CB161656
DEFINITION K-EST0221639 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-48-D07
5', mRNA sequence.

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ACCESSION CB161656
VERSION CB161656.1 GI:28147782
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 518)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

```

```

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 48 row: D column: 07
High quality sequence stop: 518.

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FEATURES
source
1..518

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L18POOL1n1-48-D07"
/cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
/lab_host="Top10F"
/clone_lib="L18POOL1n1"
/note="Organ: Liver; Vector: pTTT3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,

```

M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

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ORIGIN
Query Match      95.2%; Score 282.8; DB 6; Length 518;
Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
    |||
Db 225 CAATCGATGGGCGATCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 284

Qy 62 TTGTCAAGCTGGGCTACTTCTCATCGAGCGCGGCTTGTGCTCTTGTCTTCTTGTTC 121
    |||
Db 285 TTGTCAAGCTGGGCTACTTCTCATCGAGCGCGGCTTGTGCTCTTGTCTTCTTGTTC 344

Qy 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGACGTTCTTTCATCC 181
    |||
Db 345 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTGTGACGTTCTTTCATCC 404

Qy 182 TCCTCTCATCTTCAATGCTGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
    |||
Db 405 TCCTCTCATCTTCAATGCTGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464

Qy 242 TGGCTGAGCAGCTTCCGAGCTTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 287
    |||
Db 465 TGGCTGAGCAGCTTCCGAGCTTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 510

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RESULT 3
LOCUS CD709223
DEFINITION EST25750 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD709223
VERSION CD709223.1 GI:32239853
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

```

```

REFERENCE 1 (bases 1 to 539)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

```

```

PEATUES
source
1..539
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

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ORIGIN
Query Match      95.2%; Score 282.8; DB 6; Length 539;
Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
    |||
Db 156 CAATCGATGGGCGATCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 215

```


obtained cDNA vectors were used for transformation of competent cells E. coli Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 95.2%; Score 282.8; DB 3; Length 543;
Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 61
DB 246 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 305
QY 62 TTGTCAACGTGGGCTACTTCTCATFCGACGCGCGGTTGGTCTTTCTTGTTCCTTC 121
DB 306 TTGTCAACGTGGGCTACTTCTCATFCGACGCGCGGTTGGTCTTTCTTGTTCCTTC 365
QY 122 TGGGCTGTATGTGCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 366 TGGGCTGTATGTGCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 425
QY 182 TCCTCTCATCTTCAATGCTGAGGTTGACGCTGCTGTGCGCCCTTGGTGACACATAA 241
DB 426 TCCTCTCATCTTCAATGCTGAGGTTGACGCTGCTGTGCGCCCTTGGTGACACATAA 485
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGTGAGTGCCTGCCATCAAGAA 287
DB 486 TGGCTGAGCACTTCCCGAGTGTGCTGTGAGTGCCTGCCATCAAGAA 531

RESULT 6

CD700012
LOCUS EST16536 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003

ACCESSION CD700012
VERSION CD700012.1 GI:32229841

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 546)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)

COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
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/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

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Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 61
DB 255 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 314

QY 62 TTGTCAACGTGGGCTACTTCTCATFCGACGCGCGGTTGGTCTTTCTTGTTCCTTC 121
DB 315 TTGTCAACGTGGGCTACTTCTCATFCGACGCGCGGTTGGTCTTTCTTGTTCCTTC 374
QY 122 TGGGCTGTATGTGCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 375 TGGGCTGTATGTGCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 434
QY 182 TCCTCTCATCTTCAATGCTGAGGTTGACGCTGCTGTGCGCCCTTGGTGACACATAA 241
DB 435 TCCTCTCATCTTCAATGCTGAGGTTGACGCTGCTGTGCGCCCTTGGTGACACATAA 494
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGTGAGTGCCTGCCATCAAGAA 287
DB 495 TGGCTGAGCACTTCCCGAGTGTGCTGTGAGTGCCTGCCATCAAGAA 540

RESULT 7

BE249898
LOCUS 600942941F1 NIH MGC_15 Homo sapiens cDNA clone IMAGE:2959379 5',
DEFINITION mRNA sequence.

ACCESSION BE249898
VERSION BE249898.1 GI:9120001

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 549)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM51 row: a column: 12

High quality sequence stop: 549.
Location/Qualifiers
1..549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NIH MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

FEATURES

Location/Qualifiers
1..549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NIH MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 95.2%; Score 282.8; DB 2; Length 549;
Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 61
DB 206 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 265

QY 62 TTGTCAACGTGGGCTACTTCTCATFCGACGCGCGGTTGGTCTTTCTTGTTCCTTC 121

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Db      266  TTGTCACGTTGGGCTACTTCTCATCCAGCCGGCTTGGCTTTTGGCTCTTGGTTTCC 325
Qy      122  TGGGCTGCTATGTTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db      326  TGGGCTGCTATGTTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 385
Qy      182  TCTCTCTCATCTTCATTCGTCGAGTTGTCAGCTGCTGTGGTCGCTTGGTGACACATAA 241
Db      386  TCCTCTCTCATCTTCATTCGTCGAGTTGTCAGCTGCTGTGGTCGCTTGGTGACACCAA 445
Qy      242  TGCGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
Db      446  TGCGTGAGCACTTCTCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 491

RESULT 8
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LOCUS   K-EST0087919 S18N669761 Homo sapiens cDNA clone S18N669761-20-H08
DEFINITION
5', mRNA sequence.
ACCESSION BM819756
VERSION   BM819756.1 GI:19176169
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
          Genome Research Center
          Korea Research Institute of Bioscience & Biotechnology
          52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
          Tel: +82-42-860-4470
          Fax: +82-42-860-4409
          Email: yongseung@mail.krribb.re.kr
          Plate: 20 row: H column: 08
          High quality sequence stop: 554.
          Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="S18N669761-20-H08"
              /sex="F"
              /lab_host="Top10F'"
              /notes="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
              Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
              bacterial alkaline phosphatase (BAP) and then decapped
              with tobacco acid pyrophosphatase (TAP). The decapped
              intact mRNA was ligated with DNA-RNA linker including EcoR
              I site by treatment of T4 RNA ligase and the first strand
              cDNA was synthesized from oligo dt-selected mRNA by
              priming with dt-tailed vector. The dt-tailed vector was
              adjusted to have about 60nt. The cDNA vector was
              circularized with E. coli DNA ligase after digestion of
              EcoRI which site is also included in vector. An RNA strand
              converted to a DNA strand by Okayama-Berg method. The
              obtained cDNA vectors were used for transformation of
              competent cells E. coli Top10F' by electroporation method.
              The cDNA libraries constructed by this method are
              full-length enriched cDNA library."
FEATURES
source
ORIGIN
Query Match 95.2%; Score 282.8; DB 3; Length 554;
Best Local Similarity 99.3%; Pred. No. 3.8e-68;

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Db 234 CAATCGATGGGCGATCCTTTCTGAAGATCTTTCGGGCCACTGTGTCAGTGCCATGCAGT 293

Qy 62 TTGTCAACGTGGGCGTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTTCC 121

Db 294 TTGTCAACGTGGGCGTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTTCC 353

Qy 122 TGGGCTGTATGTGTCTAAGACTGAGACCAAGTGTGCCCTCGTGCAGCTTCTTCTTCATCC 181

Db 354 TGGGCTGTATGTGTCTAAGACTGAGACCAAGTGTGCCCTCGTGCAGCTTCTTCTTCATCC 413

Qy 182 TCCTCTCATCTTCAATGCTGAGGTGCAGCTGTGGTGTGCCCTTGGTGTACACCATAA 241

Db 414 TCCTCTCATCTTCAATGCTGAGGTGTGCAGCTGTGGTGTGCCCTTGGTGTACACCATAA 473

Qy 242 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGTGCCCTGCCATCAAGAA 287

Db 474 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGTGCCCTGCCATCAAGAA 519

RESULT 10

BG428609

LOCUS

DEFINITION

602494743F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608394 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 564)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCW1350 row: f column: 11

High quality sequence stop: 560.

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4608394"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1: Sfil (ggcgcttcggc); Site: 2: Sfil (ggcattatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

FEATURES

Source

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4608394"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1: Sfil (ggcgcttcggc); Site: 2: Sfil (ggcattatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.2%; Score 282.8; DB 2; Length 564;

Best Local Similarity 99.3%; Pred. No. 3.9e-68;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTTCGGGCCACTGTGTCAGTGCCATGCAGT 61

Db 233 CAATCGATGGGCGATCCTTTCTGAAGATCTTTCGGGCCACTGTGTCAGTGCCATGCAGT 292

Qy 62 TTGTCAACGTGGGCGTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTTCC 121

Db 293 TTGTCAACGTGGGCGTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTTCC 352

Qy 122 TGGGCTGTATGTGTCTAAGACTGAGACCAAGTGTGCCCTCGTGCAGCTTCTTCTTCATCC 181

Db 353 TGGGCTGTATGTGTCTAAGACTGAGACCAAGTGTGCCCTCGTGCAGCTTCTTCTTCATCC 412

Qy 182 TCCTCTCATCTTCAATGCTGAGGTGCAGCTGTGGTGTGCCCTTGGTGTACACCATAA 241

Db 413 TCCTCTCATCTTCAATGCTGAGGTGTGCAGCTGTGGTGTGCCCTTGGTGTACACCATAA 472

Qy 242 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGTGCCCTGCCATCAAGAA 287

Db 473 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGTGCCCTGCCATCAAGAA 518

RESULT 11

BM819724

LOCUS

DEFINITION

X-EST0087883 S18N669761 Homo sapiens cDNA clone S18N669761-20-E08 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 566)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 20 row: E column: 08

High quality sequence stop: 566.

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S18N669761-20-E08"

/sex="F"

/lab_host="Top10F"

/clone_lib="S18N669761"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

FEATURES

Source

1..566

/organism="Homo sapiens"

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/clone="S18N669761-20-E08"

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/lab_host="Top10F"

/clone_lib="S18N669761"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN


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Query Match          95.2%; Score 282.8; DB 3; Length 566;
Best Local Similarity 99.3%; Pred. No. 3.9e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTCTCCAGTGCCATGCAGT 61
Db 232 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTCTCCAGTGCCATGCAGT 291

Qy 62 TTGTCAACGTGGGGTACTTCTCTCATCGCAGCCGCGTGTGGTCTTGGTCTTGGTTTCC 121
Db 292 TTGTCAACGTGGGGTACTTCTCTCATCGCAGCCGCGTGTGGTCTTGGTCTTGGTTTCC 351

Qy 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 352 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 411

Qy 182 TCCTCTCATCTTCAATGCTGAGTTGCGAGTGTGCTGTGGTCCCTTGGTGTACACCAATAA 241
Db 412 TCCTCTCATCTTCAATGCTGAGTTGCGAGTGTGCTGTGGTCCCTTGGTGTACACCAATAA 471

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db 472 TGGCTGAGCACTTCTCGACGTTGCTGTAGTGCCTGCCATCAAGAA 517

RESULT 12
BP261193          568 bp mRNA linear EST 16-SEP-2004
LOCUS
DEFINITION BP261193 Sugano cDNA library, small intestine Homo sapiens cDNA
ACCESSION BP261193
VERSION BP261193.1 GI:52176424
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 568)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. 568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTCTCCAGTGCCATGCAGT 61.
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Db 298 TTGTCAACGTGGGGTACTTCTCTCATCGCAGCCGCGTGTGGTCTTGGTCTTGGTTTCC 357

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Qy 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 358 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 417

Qy 182 TCCTCTCATCTTCAATGCTGAGTTGCGAGTGTGCTGTGGTCCCTTGGTGTACACCAATAA 241
Db 418 TCCTCTCATCTTCAATGCTGAGTTGCGAGTGTGCTGTGGTCCCTTGGTGTACACCAATAA 477

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db 478 TGGCTGAGCACTTCTCGACGTTGCTGTAGTGCCTGCCATCAAGAA 523

RESULT 13
BP262643          568 bp mRNA linear EST 16-SEP-2004
LOCUS
DEFINITION BP262643 Sugano cDNA library, small intestine Homo sapiens cDNA
ACCESSION BP262643
VERSION BP262643.1 GI:52177874
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 568)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. 568
/organism="Homo sapiens"
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/clone_lib="Sugano cDNA library, small intestine"

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Best Local Similarity 99.3%; Pred. No. 3.9e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCCACTGTCTCCAGTGCCATGCAGT 61
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Qy 62 TTGTCAACGTGGGGTACTTCTCTCATCGCAGCCGCGTGTGGTCTTGGTCTTGGTTTCC 121
Db 293 TTGTCAACGTGGGGTACTTCTCTCATCGCAGCCGCGTGTGGTCTTGGTCTTGGTTTCC 352

Qy 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 353 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 412

Qy 182 TCCTCTCATCTTCAATGCTGAGTTGCGAGTGTGCTGTGGTCCCTTGGTGTACACCAATAA 241
Db 413 TCCTCTCATCTTCAATGCTGAGTTGCGAGTGTGCTGTGGTCCCTTGGTGTACACCAATAA 472

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db 473 TGGCTGAGCACTTCTCGACGTTGCTGTAGTGCCTGCCATCAAGAA 518

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RESULT 14	BM819701	571 bp	mRNA	linear	EST 06-MAR-2002			
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ACCESSION	BM819701							
VERSION	BM819701.1	GI:19176114						
KEYWORDS	EST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1 (bases 1 to 571)							
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.							
TITLE	21C Frontier Korean EST Project 2001							
JOURNAL	Unpublished (2002)							
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongaung@mail.krrib.re.kr Plate: 20 row: C column: 03 High quality sequence stop: 571.							
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	/sex="F"							
	/lab_host="Top10F"							
	/clone_lib="S18N669761"							
	/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."							
ORIGIN								
Query Match	95.2%; Score 282.8; DB 3; Length 571;							
Best Local Similarity	99.3%; Pred. No. 3.9e-68;							
Matches	284;	Conservative	0;	Mismatches	2; Indels 0; Gaps 0;			
Qy	2	CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCAGTGCATGCAGT	61					
Db	237	CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCAGTGCATGCAGT	296					
Qy	62	TTGTCACTGGGGTACTTCTCATCCGACCGCGGTGGTCTTTGCTCTGGTTTCC	121					
Db	297	TTGTCAACAGTGGGGTACTTCTCATCGACCGCGGTGGTCTTTGCTCTGGTTTCC	356					
Qy	122	TGGGCTGCTATGGTGCTAAGACTCAGACGAAGTGTGCCTCGTCGACGTTCTTCTTCATCC	181					
Db	357	TGGGCTGCTATGGTGCTAAGACTCAGACGAAGTGTGCCTCGTCGACGTTCTTCTTCATCC	416					
Qy	182	TCCTCCTCATCTTCATTGCTGAGGTTGCAGTGTCTGTGGTGCCTTGGTGACACCATAA	241					

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 11:09:33 ; Search time 2131 Seconds
(without alignments)
7922.339 Million cell updates/sec

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Perfect score: 297
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pt.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	6	A91802 Sequence 1
2	297	100.0	297	6	BD023236 DNA for e
3	282.8	95.2	513	6	AX079459 Sequence
c 4	282.8	95.2	635	6	AX193458 Sequence
5	282.8	95.2	792	6	AX379319 Sequence
6	282.8	95.2	933	6	BD070552 Novel hum
7	282.8	95.2	1044	8	AF133425 Homo sapi
8	282.8	95.2	1076	6	CQ896240 Sequence
9	282.8	95.2	1076	8	AF054838 Homo sapi
10	282.8	95.2	1077	6	CQ719831 Sequence
11	282.8	95.2	1278	8	AF065388 Homo sapi
12	282.8	95.2	1288	6	BD069061 Polynucle
c 13	282.8	95.2	1288	6	BD069078 Polynucle
14	282.8	95.2	1289	6	BD070259 Compounds
15	282.8	95.2	1289	6	BD242023 Compounds
16	282.8	95.2	1289	6	AR237206 Sequence
17	282.8	95.2	1289	6	AR278230 Sequence
18	282.8	95.2	1289	6	AR366926 Sequence

19	282.8	95.2	1289	6	AR370822 Sequence
20	282.8	95.2	1289	6	AR392327 Sequence
21	282.8	95.2	1289	6	AR399962 Sequence
22	282.8	95.2	1289	6	AR405229 Sequence
23	282.8	95.2	1289	6	AR439433 Sequence
24	282.8	95.2	1289	6	AR563609 Sequence
25	282.8	95.2	1289	6	AR588595 Sequence
26	282.8	95.2	1289	6	AR605415 Sequence
27	282.8	95.2	1289	6	AR653029 Sequence
28	282.8	95.2	1289	6	AR656754 Sequence
29	282.8	95.2	1289	6	AX106213 Sequence
30	282.8	95.2	1289	6	AX106330 Sequence
31	282.8	95.2	1289	6	AX140621 Sequence
32	282.8	95.2	1289	6	AX200481 Sequence
33	282.8	95.2	1289	6	AX267137 Sequence
34	282.8	95.2	1297	8	BC007290 Homo sapi
35	282.8	95.2	1297	8	BC013404 Homo sapi
36	282.8	95.2	1324	6	BD195620 70 human
37	282.8	95.2	1324	6	CQ775665 Sequence
38	282.8	95.2	1324	6	AR352675 Sequence
39	282.8	95.2	1324	6	AR650285 Sequence
40	282.8	95.2	1376	6	BD195552 70 human
41	282.8	95.2	1376	6	CQ775597 Sequence
42	282.8	95.2	1376	6	AR352607 Sequence
43	282.8	95.2	1376	6	AR650217 Sequence
44	282.8	95.2	1533	6	BD228312 Method of
45	282.8	95.2	1533	6	AR678455 Sequence

ALIGNMENTS

RESULT 1
A91802
LOCUS A91802 297 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9823775.
ACCESSION A91802
VERSION A91802.1 GI:6740681

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

unidentified
unclassified sequences.
1 (bases 1 to 297)
Nees, M. and Duerst, M.
DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
Patent: WO 9823775-A 1 04-JUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)

Location/Qualifiers
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CDS

ORIGIN

Query Match 100.0%; Score 297; DB 6; Length 297;
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Db 1 GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCTGCATGCATGCAG 60
Qy 61 TTTGTCAACCTGGGCTACTTCTCTCATCGACCGCGGCTTGTGCTCTTGTCTTCTGTTTC 120
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Qy	121	CTGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCTTCATC	180
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Qy	181	CTCCTCCCTCATCTTCATTTGCTGAGGTTGCGAGCTGCTGTGGTGCGCTTGGGTACACCAT	240
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Qy	241	ATGGGCTGAGCACTTCCCGACGTTGCTGTGTAGTGCCTGCCATCAAGAAGATTATGGTT	297
Db	241	ATGGGCTGAGCACTTCCCGACGTTGCTGTGTAGTGCCTGCCATCAAGAAGATTATGGTT	297
RESULT 2			
BD023236			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominoidea; Homo.			
REFERENCE			
1 (bases 1 to 297)			
Durst,M. and Ness,M.			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FN JP 2001504703-A/1			
PD 10-APR-2001			
PF 12-NOV-1997 JP 1998524127			
PR 27-NOV-1996 DE 19649207.6			
PI MATHIAS DURUST MATHIAS NESS			
PC C12N15/09, C07K14/00, C07K16/00, C12P21/02, C12Q1/68, C12Q1/70, PC			
G01N33/574,			
PC C12N15/00			
CC Strandedness: Double;			
CC Topology: Linear;			
FH Key			
FT CDS			
Location/Qualifiers			
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Best Local Similarity			
Matches			
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0; Mismatches			
0; Indels			
0; Gaps			
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Db	1	GCAATCGATGGGSCATCCCTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCATGCAG	60
Qy	61	TTTGTCAACGTCGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTTGGCTTTTC	120
Db	61	TTTGTCAACGTCGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTTGGCTTTTC	120
Qy	121	CTGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCTTCATC	180
Db	121	CTGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCTTCATC	180
Qy	181	CTCCTCTCATCTTCATTTGCTGAGGTTGCGAGCTGCTGTGGTGCGCTTGGGTACACCAT	240
Db	181	CTCCTCTCATCTTCATTTGCTGAGGTTGCGAGCTGCTGTGGTGCGCTTGGGTACACCAT	240
Qy	241	ATGGCTGAGCACTTCCCGACGTTGCTGTGTAGTGCCTGCCATCAAGAAGATTATGGTT	297
Db	241	ATGGCTGAGCACTTCCCGACGTTGCTGTGTAGTGCCTGCCATCAAGAAGATTATGGTT	297

RESULT 3					
AX079459	Sequence 203 from Patent WO0107611.	513 bp	DNA	linear	PAT 22-FEB-2001
LOCUS					
DEFINITION					
ACCESSION	AX079459				
VERSION	AX079459.1	GI:13159019			
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
AUTHORS	Baker,K.P., Goddard,A. and Wood,W.I.				
TITLE	Human polypeptides and methods for the use thereof				
JOURNAL	Patent: WO 0107611-A 203 01-FEB-2001;				
	Genentech, Inc. (US)				
FEATURES	Location/Qualifiers				
source	1..513				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
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	Best Local Similarity	99.3%;	Fred. No. 1.7e-61;		
	Matches 284;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	2 CAATCGATGGGCGCATCTTTCTGAAGATCTTCGGGGCCACTGTGTCGCAGTGCATGCAGT 61				
Db	99 CAATCGATGGGCGCATCTTTCTGAAGATCTTCGGGGCCACTGTGTCGCAGTGCATGCAGT 158				
Qy	62 TTGTCAACGTGGGCTACTTCTCATCGACGCCGGCTTGFGTCTTTGCTCTTGGTTTCC 121				
Db	159 TTGTCAACGTGGGCTACTTCTCATCGACGCCGGCTTGFGTCTTTGCTCTTGGTTTCC 218				
Qy	122 TGGGCTGCTATGGTGCTTAGACCTGAGCAGAAGTGCCCTCGTACGCTTCTTTTCATCC 181				
Db	219 TGGGCTGCTATGGTGCTTAAGACTGAGACGAAGTGGCCCTCGTACGCTTCTTTTCATCC 278				
Qy	182 TCCTCTCATCTTTCATTGCTGAGGTGCAGCTGCTGTGTCGCTTGGTGACACCATAA 241				
Db	279 TCCTCTCATCTTTCATTGCTGAGGTGCAGCTGCTGTGTCGCTTGGTGACACCATAA 338				
Qy	242 TGCGTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287				
Db	339 TGCGTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 384				
RESULT 4					
AX193458/c	Sequence 1025 from Patent WO0149716.	635 bp	DNA	linear	PAT 15-AUG-2001
LOCUS					
DEFINITION					
ACCESSION	AX193458				
VERSION	AX193458.1	GI:15211409			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
AUTHORS	Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.				
TITLE	Compounds for immunotherapy and diagnosis of colon cancer and methods for their use				
JOURNAL	Patent: WO 0149716-A 1025 12-JUL-2001;				
	CORIXA CORPORATION (US)				
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/db_xref="taxon:9606"

ORIGIN

Query Match 95.2%; Score 282.8; DB 6; Length 635;
Best Local Similarity 99.3%; Pred. No. 1.7e-61;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCATGCAGT 61
Db 575 CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCATGCAGT 516

Qy 62 TTGTCAACGTGGGCTACTCTCTCATCGCAGCCGGCTGTGGTCTTGTCTTGGTTTCC 121
Db 515 TTGTCAACGTGGGCTACTCTCTCATCGCAGCCGGCTGTGGTCTTGTCTTGGTTTCC 456

Qy 122 TGGGCTGCTATGGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 181
Db 455 TGGGCTGCTATGGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 396

Qy 182 TCCTCCTCATCTTCAATGCTGAGGTTCGAGTGTGCTGTGGTGGCTTGGTGACACCAAA 241
Db 395 TCCTCCTCATCTTCAATGCTGAGGTTCGAGTGTGCTGTGGTGGCTTGGTGACACCAAA 336

Qy 242 TGGGTGAGCACTTCCCGAGTGTGTGAGTGTGCTGTGCCATCAAGAA 287
Db 335 TGGGTGAGCACTTCCCGAGTGTGTGAGTGTGCTGTGCCATCAAGAA 290

RESULT 5
AX379319
LOCUS AX379319 792 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 361 from Patent WO0196389.
ACCESSION AX379319
VERSION AX379319.1 GI:19575159
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS Mesgher, M.J., King, G.E., Xu, J. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0196389-A 361 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..792
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 95.2%; Score 282.8; DB 6; Length 792;
Best Local Similarity 99.3%; Pred. No. 1.7e-61;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCATGCAGT 61
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Qy 62 TTGTCAACGTGGGCTACTCTCTCATCGCAGCCGGCTGTGGTCTTGTCTTGGTTTCC 121
Db 274 TTGTCAACGTGGGCTACTCTCTCATCGCAGCCGGCTGTGGTCTTGTCTTGGTTTCC 333

Qy 122 TGGGCTGCTATGGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 181
Db 334 TGGGCTGCTATGGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 393

Qy 182 TCCTCCTCATCTTCAATGCTGAGGTTCGAGTGTGCTGTGGTGGCTTGGTGACACCAAA 241
Db 394 TCCTCCTCATCTTCAATGCTGAGGTTCGAGTGTGCTGTGGTGGCTTGGTGACACCAAA 453

Qy 242 TGGCTGAGCACTTCCCGAGTGTGTGAGTGTGCTGCCATCAAGAA 287
Db 454 TGGCTGAGCACTTCCCGAGTGTGTGAGTGTGCTGCCATCAAGAA 499

RESULT 6
BD070552
LOCUS BD070552 933 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel human tumor-associated antigen.
ACCESSION BD070552
VERSION BD070552.1 GI:22616155
KEYWORDS JP 2001515349-A/1.
SOURCE unclassified
ORGANISM unclassified.

REFERENCE
AUTHORS Hillman, J.L. and Goli, S.K.
TITLE Novel human tumor-associated antigen
JOURNAL Patent: JP 2001515349-A 1 18-SEP-2001;
INCYTE PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2001515349-A/1
PD 18-SEP-2001
PF 27-FEB-1998 JP 1998537919
PR 28-FEB-1997 US 08/808148
PI JENNIFER L HILLMAN, SURYA K GOLI
PC C12N15/12, C07K14/705, A61K38/12, C07K16/28, G01N33/50 CC
Strandedness: Single;

CC Topology: Linear;
CC Novel human tumor-associated antigen
FH Key Location/Qualifiers
FT source 1..933
FT /organism="Unidentified".
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source Location/Qualifiers
1..933
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 95.2%; Score 282.8; DB 6; Length 933;
Best Local Similarity 99.3%; Pred. No. 1.7e-61;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCATGCAGT 61
Db 225 CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTGCATGCAGT 284

Qy 62 TTGTCAACGTGGGCTACTCTCTCATCGCAGCCGGCTGTGGTCTTGTCTTGGTTTCC 121
Db 285 TTGTCAACGTGGGCTACTCTCTCATCGCAGCCGGCTGTGGTCTTGTCTTGGTTTCC 344

Qy 122 TGGGCTGCTATGGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 181
Db 345 TGGGCTGCTATGGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 404

Qy 182 TCCTCCTCATCTTCAATGCTGAGGTTCGAGTGTGCTGTGGTGGCTTGGTGACACCAAA 241
Db 405 TCCTCCTCATCTTCAATGCTGAGGTTCGAGTGTGCTGTGGTGGCTTGGTGACACCAAA 464

Qy 242 TGGCTGAGCACTTCCCGAGTGTGTGAGTGTGCTGCCATCAAGAA 287
Db 465 TGGCTGAGCACTTCCCGAGTGTGTGAGTGTGCTGCCATCAAGAA 510

RESULT 7
AF133425
LOCUS AF133425 1044 bp mRNA linear PRI 16-NOV-1999
DEFINITION Homo sapiens tetraepanin TM4-C mRNA, complete cds.
ACCESSION AF133425
VERSION AF133425.1 GI:6434903
KEYWORDS Homo sapiens (human)
SOURCE

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:33:09 ; Search time 18.8419 Seconds

(without alignments)
2224.208 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

Sequence: 1 gcaatcgatgggcacccctt.....ccatcaagaagattatgggtt 297

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=UniProt -QMT=fastcan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	80.3	241	1 TSNI1_HUMAN	O60635 homo sapien
2	453	80.3	241	2 QSVST0_HUMAN	QSVST0 homo sapien
3	450	79.8	241	1 TSNI1_PONPY	Q3rc27 pongo pygma
4	442	78.4	240	2 Q47W6_MACFA	Q47W6 macaca fasc
5	371	65.8	240	2 Q99J59_MOUSE	Q99J59 mus musculus
6	366	64.9	241	2 Q6AYR9_RAT	Q6AYR9 rattus norv
7	273.5	48.5	244	2 QSHZS3_XENLA	QSHZS3 xenopus lae
8	270.5	48.0	244	2 Q6DDY1_XENLA	Q6DDY1 xenopus lae
9	221	39.2	240	2 Q6P420_XENLA	Q6P420 xenopus lae
10	210.5	37.3	234	2 Q7T2B8_BRARE	Q7T2B8 brachydanio
11	161	28.5	246	2 Q4RSJ3_TETNG	Q4RSJ3 tetraodon n
12	158	28.0	225	2 Q569S1_XENLA	Q569S1 xenopus lae
13	158	28.0	247	2 Q9PT80_CHICK	Q9PT80 gallus gall
14	157.5	27.9	246	2 Q6DH56_BRARE	Q6DH56 brachydanio
15	157	27.8	247	2 Q6GP44_XENLA	Q6GP44 xenopus lae
16	157	27.8	265	2 Q802B9_XENLA	Q802B9 xenopus lae

17	155	27.5	249	1 TSNI1_BOVIN	Q58CY8 bos taurus
18	154.5	27.4	235	2 Q4S1G3_TETNG	Q4S1G3 tetraodon n
19	153	27.1	248	1 TSNI1_HUMAN	Q96S18 homo sapien
20	153	27.1	267	2 Q8WU1_HUMAN	Q8WU1 homo sapien
21	152.5	27.0	241	2 Q6DSC4_BRARE	Q6DSC4 brachydanio
22	151.5	26.9	231	2 Q5XGS2_XENLA	Q5XGS2 xenopus lae
23	149.5	26.5	238	1 TSNI1_HUMAN	Q14817 homo sapien
24	149.5	26.5	238	2 Q6IAP6_HUMAN	Q6IAP6 homo sapien
25	149.5	26.5	238	1 Q5RAP3_PONPY	Q5RAP3 pongo pygma
26	147.5	26.2	238	1 TSNI1_MOUSE	Q9CDK3 mus musculus
27	147.5	26.2	238	2 Q5BK80_RAT	Q5BK80 rattus norv
28	147.5	26.2	238	2 Q4FWU7_MOUSE	Q4FWU7 mus musculus
29	146.5	26.0	218	1 CD53_RAT	Q24495 rattus norv
30	145.5	25.8	218	1 CD53_MOUSE	Q61451 mus musculus
31	145.5	25.8	248	1 TSNI1_MOUSE	Q80W1 mus musculus
32	144	25.5	217	2 Q6DCU4_XENLA	Q6DCU4 xenopus lae
33	143	25.4	236	2 Q9DSU7_BRARE	Q9DSU7 brachydanio
34	143	25.4	236	2 Q6PFU1_BRARE	Q6PFU1 brachydanio
35	141	25.0	211	2 Q9GLG9_SAGOE	Q9GLG9 saguinus oe
36	141	25.0	236	1 CD81_CERAE	Q97703 cercopithec
37	141	25.0	236	1 CD81_HUMAN	P60033 homo sapien
38	141	25.0	236	1 CD81_MOUSE	P35762 mus musculus
39	141	25.0	236	1 CD81_PANTR	P60034 pan troglod
40	141	25.0	236	1 CD81_RAT	Q62745 rattus norv
41	141	25.0	236	1 CD81_SAGOE	Q9N019 saguinus oe
42	141	25.0	236	2 Q5U0J6_HUMAN	Q5U0J6 homo sapien
43	141	25.0	236	2 Q7YR89_9EUTH	Q7YR89 tupia chin
44	141	25.0	236	2 Q91V78_MOUSE	Q91V78 mus musculus
45	141	25.0	236	2 Q6P9V1_RAT	Q6P9V1 rattus norv

ALIGNMENTS

RESULT 1

TSNI1_HUMAN
ID TSNI1_HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tetraspanin-1 (Tsban-1) (Tetraspanin NET-1) (Tetraspanin TM4-C).
GN Names=TSBAN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TWASF family";
RL Blochim. Biophys. Acta 1399:101-104 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Pule K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspanins";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon;
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OC NCBI_TaxID=9600;
 RN (1)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE: Kidney;
 RG The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; CR858455; CAH90683.1; -; mRNA.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspanin; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Transmembrane.
 FT TOPO_DOM 1 11
 FT TRANSMEM 12 34
 FT TOPO_DOM 35 53
 FT TRANSMEM 54 76
 FT TOPO_DOM 77 88
 FT TRANSMEM 89 111
 FT TOPO_DOM 112 214
 FT TRANSMEM 215 237
 FT TOPO_DOM 238 241
 FT CARBOHYD 141 141
 FT CARBOHYD 154 154
 FT CARBOHYD 178 178
 FT CARBOHYD 184 184
 SQ SEQUENCE 241 AA; 26341 MW; BE029CDAD83F1139 CRC64;
 Alignment Scores:
 Pred. No.: 3,116-38 Length: 241
 Score: 450.00 Matches: 92
 Percent Similarity: 97.9% Conservative: 2
 Best Local Similarity: 95.8% Mismatches: 2
 Query Match: 79.8% Indels: 0
 DB: 1 Gaps: 0
 US-10-079-954-1 (1-297) x TSN1_PONPY (1-241)
 QY 1 GCAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAG 60
 Db 33 SerleaspglyalaSerPheLeuylslePheGlyProleuSerSerSerAlaMetGln 52
 QY 61 TTGTGCAACGTGGGCTACTTCTCATCGACGCGCGTGTGTCCTTGTCTTCTTCTTC 120
 Db 53 PheValAsnValGlyTyrrPheLeulleAlaAlaGlyValValPheAlaLeuGlyPhe 72
 QY 121 CTGGGCTCTATGCTGCTAGACTGAGAGTGCAGTGCCTGCTGCTGCTGCTGCTGCT 180
 Db 73 LeuGlyCysTyrrGlyAlaGlnThrGluSerLysCysAlaLeuMetThrPhePhePhe 92
 QY 181 CTCTCTCTCATCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 240
 Db 93 LeuLeuLeullePheilleAlaGluValAlaAlaValValAlaLeuValTyrrThr 112
 QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
 Db 113 MetAlaGluHiePheLeuThrLeuLeuValValProAlaIleLysLys 128
 RESULT 4
 Q4R7W6_MACFA PRELIMINARY; PRT; 240 AA.

Q4R7W6;
 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Testis cDNA clone: QtsA-14223, similar to human tetraspan 1 (TSPAN-1).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopitheinae; Macaca.
 OX NCBI_TaxID=9541;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA International consortium for macaque cDNA sequencing, analysis;
 RT "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB168695; BAB0806.1; -; mRNA.
 SQ SEQUENCE 240 AA; 26243 MW; 5AB106570E958D3F CRC64;
 Alignment Scores:
 Pred. No.: 2,146-37 Length: 240
 Score: 442.00 Matches: 90
 Percent Similarity: 96.9% Conservative: 3
 Best Local Similarity: 93.8% Mismatches: 3
 Query Match: 78.4% Indels: 0
 DB: 2 Gaps: 0
 US-10-079-954-1 (1-297) x Q4R7W6_MACFA (1-240)
 QY 1 GCAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCATGCAG 60
 Db 33 SerleaspglyalaSerPheLeuylslePheGlyProleuSerSerSerAlaMetGln 52
 QY 61 TTGTGCAACGTGGGCTACTTCTCATCGACGCGCGTGTGTCCTTGTCTTCTTCTTC 120
 Db 53 PheValAsnValGlyTyrrPheLeulleAlaAlaGlyValValPheAlaLeuGlyPhe 72
 QY 121 CTGGGCTCTATGCTGCTAGACTGAGAGTGCAGTGCCTGCTGCTGCTGCTGCTGCT 180
 Db 73 LeuGlyCysTyrrGlyAlaGlnThrGluSerLysCysAlaLeuMetThrPhePhePhe 92
 QY 181 CTCTCTCTCATCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 240
 Db 93 LeuLeuLeullePheilleAlaGluValAlaAlaValValAlaLeuValTyrrThr 112
 QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
 Db 113 MetAlaGluHiePheLeuThrLeuLeuValValProAlaIleLysLys 128
 RESULT 5
 Q99J59_MOUSE PRELIMINARY; PRT; 240 AA.
 ID Q99J59_MOUSE
 AC Q99J59;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Tetraspan 1 (Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030418M05 product:similar to tetraspan TSPAN-1).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR002229; RhesusRHD.
DR Pfam; PF000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; I.
DR PRINTS; PR00342; RHESUSRHD.
DR PRINTS; PR00259; TMPOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR SQ SEQUENCE 241 AA; 26453 MW; 9118E865464D1A70 CRC64;

Alignment Scores:
Pred. No.: 2e-29 Length: 241
Score: 366.00 Matches: 73
Percent Similarity: 85.4% Conservative: 9
Best Local Similarity: 76.0% Mismatches: 14
Query Match: 64.9% Indels: 0
DB: 2 Gaps: 0

US-10-079-954-1 (1-297) x Q6AYR9_RAT (1-241)
QY 1 GCAATCGATGGGCACTCCTTTCTGAAGACTCTTCGGGCCACTGTGCTCCAGTGCCCATGCAG 60
Db :
Db 33 SerValAspGlyThrSerPheLeuLysAlaPheGlySerLeuSerSerAlaMetGln 52
QY 61 TTTGTCAACGTGGGTACTTCTCCTCATCGCAGCGCGCGTGTGGTCTTGTCTCTGGTTC 120
Db PheValAsnValGlyTyrrPheLeuIleAlaAlaGlyAlaValLeuPheIleLeuGlyPhe 72
Db 53 PheValAsnValGlyTyrrPheLeuIleAlaAlaGlyAlaValLeuPheIleLeuGlyPhe 72
QY 121 CTGGGCTGCTATGCTGCTAAAGACTGAGACAAGTGCCTCGTAGCGTCTCTTCATC 180
Db :
Db 73 LeuGlyCysTyrrGlyAlaHisSerGluAsnLysCysValLeuMetMetPhePheSerIle 92
QY 181 CTCCTCTCATCTTCATTGCTGAGAGTTCAGAGTCTGCTGGTGCCTGGTGTACACCATA 240
Db :
Db 93 LeuLeuIleIlePheIleAlaGluIleAlaGlyAlaValAlaLeuValTyrrThr 112
QY 241 ATGGCTGAGCACATTCCGACGTTGCTGGTAGTGCTGCCATCAAAGAAG 288
Db 113 MetAlaGluGlnPheLeuThrPheLeuValValProAlaIleGluLys 128

RESULT 7
QSHZS3_XENLA PRELIMINARY; PRT; 244 AA.
ID QSHZS3_XENLA PRELIMINARY; AC
OS QSHZS3; AC
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC496318 protein.
GN Names=LOC496318;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RS TISSUE=Egg;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Straube R.G., Wagner L., Wagner J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RA initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RS TISSUE=Egg;
RC MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.B., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

SQ SEQUENCE 234 AA; 24894 MW; E713846FE750C054 CRC64;

Alignment Scores:

Pred. No.: 4.03e-13 Length: 234
Score: 210.50 Matches: 48
Percent Similarity: 60.6% Conservative: 12
Best Local Similarity: 48.5% Mismatches: 36
Query Match: 37.3% Indels: 3
DB: 2 Gaps: 1

US-10-079-954-1 (1-297) x Q7T2B8_BRARE (1-234)

```
QY 4 ATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTG-----TCGTCCAGTGCC 54
Db ValAspAeNglyserileLeuasnPheMetGlnSerLeuProGlyAlaserSerGlnMet 44
QY 55 ATCGAGTTTGTCAACGTGGGTACTTCTCATCGAGCGCGGGTGTGTGCTTCTT 114
Db GlyGlnValLeuasnValGlyTyrlLeuLeuAlaLeuGlyAlaValValLeu 64
QY 115 GGTTCCTGGGTGCTATGGTGAAGACTGAGACAAAGTGCCTCGTACGTTCTTC 174
Db GlyPheLeuGlyCysGlyAlaileLysGluSerArgCysMetLeuMetLeuPhePhe 84
QY 175 TTCATCTCTCTCATCTTCTGAGGTTCAGCTGCTGTGTGCTGCTGCTGTGTAC 234
Db IleIleIleLeuIleIlePheIleAlaGluValAlaGlyAlaIleValIleLeuAlaPhe 104
QY 235 ACCATAATGGCTGAGCACTTCCCGACGTTGTGTGTGCTGCTGCCATCAAGAAGATT 291
Db ArgProLeuAlaGluThrLeuIleLysGlnLeuGlyValAspAlaValLysSerLeu 123
```

RESULT 11

```
ID Q4RSA3_TETNG PRELIMINARY; PRT; 246 AA.
AC Q4RSA3
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome 13 SCAP15000, whole genome shotgun sequence.
GN ORFNames=GSTENG00029794001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN (1)
RP NUCLEOTIDE SEQUENCE.
```

```
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaut S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bionnet C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RA Nature 431:946-957(2004).
```

[2]

RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: the sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; CAAB01015000; CAG08729.1; -; Genomic DNA.
SQ SEQUENCE 246 AA; 27564 MW; AD91A3397819D50A CRC64;

Alignment Scores:

Pred. No.: 6.29e-08 Length: 246
Score: 161.00 Matches: 34
Percent Similarity: 66.3% Conservative: 23
Best Local Similarity: 39.5% Mismatches: 23
Query Match: 28.5% Indels: 6
DB: 2 Gaps: 3

US-10-079-954-1 (1-297) x Q4RSA3_TETNG (1-246)

```
QY 4 ATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCATGATTT 63
Db ValAspProThrGlyPheArgGluIle-----IleAlaAlaAsnProLeuPhe 52
QY 64 GTCACGTGGGTACTTCTCATCGAGCGCGGGTGTGTGCTTCTTGTGTTCTCTG 123
Db ThrGlyVal---TyrValIleLeuGlyLeuGlyMetLeuPheLeuGlyPheLeu 71
QY 124 GGCTGCTATGCTGAAGACTGAGACAAAGTGTGCCCTCGAGCTTCTTCTTCATCTC 183
Db GlyCysGlyAlaIleLeuArgGluAsnLysCysLeuLeuPhePheMetLeuIle 91
QY 184 CTCCTCATCTTCTCATGCTGAGTTGTCAGCTGCTGTGTGCTGCTGCTGTACACC----- 237
Db LeuLeuIlePheLeuAlaGluLeuAlaAlaIleLeuAlaPheIlePheArgGluHis 111
QY 238 ATAATGGCTGAGCACTTC 255
Db LeuThrArgGluTyrPhe 117
```

RESULT 12

```
ID Q569S1_XENLA PRELIMINARY; PRT; 225 AA.
AC Q569S1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
```

[2]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Score: 159.00 Matches: 31
Percent Similarity: 67.5% Conservative: 21
Best Local Similarity: 40.3% Mismatches: 21
Query Match: Indels: 4
DB: Gaps: 2

US-10-079-954-1 (1-297) x Q9PTE0_CHECK (1-247)

QY 4 ATCGATGGGCGCATCTTTTCTGAAGATCTTCGGGCGCACTGTCTCCAGTGCCATGCAGTTT 63
:::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 36 ValaspProThrGlyPheArgGlulle-----ValAlaAAsnProLeuLeuPhe 52

QY 64 GTCAACGTGGGTACTTCTCCTCATCGACGCCGGTGTGGCTTGTCTTGGCTTGGTTCTG 12
||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 ThrGly--Alaty-fileMetLeuAlaMetGliAlaMetLeuPheLeuGlyPheLeu 71

QY 124 GGCTGCTATGGTCTAAAGACTCAGACGAGTGTCGCCCTGGTAGCTTCTTTCATCTCTC 28
||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 GlyCyCsGlyAlaAlaIargGluAsnLysCysLeuLeuLeuPhePheMetPheille 91

QY 184 CTCCTCATCTTCTATTGCTGAGCTGCTGCGCTGTGTGGTCGCTTGGTGTAC 234
||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 92 LeuLeullePheLeuAlaGluLeuSerAlaalleLeuAlaPheillePhe 108

RESULT 14

G6DH58 BRARE
ID Q6DH58 BRARE PRELIMINARY; PRT; 246 AA.

AC Q6DH58;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Zgc:92637.
ORFNames=zgc:92637;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio;
NCBI_TaxId=7955;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Eye;
RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076124; RAH76124.1; -; mRNA.
DR ZFIN; ZDB-GENE-040718-137; zgc:92637.
DR GO; GO:0015021; C:integral to membrane; IEA.
DR GO; GO:0005764; C:lipoosome; IEA.
DR InterPro; IPR000264; Serum albumin.
DR InterPro; IPR000301; Transmem 4.

Search completed: March 23, 2006, 12:45:51
Job time : 98.2097 secs